

Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to: Welch JS, Petti AA, Miller CA, et al. *TP53 and decitabine in acute myeloid leukemia and myelodysplastic syndromes*. N Engl J Med 2016;375:2023-36. DOI: 10.1056/NEJMoa1605949

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Supplement to: Welch, JS, Petti, AA, Miller, CA, *et al.* *TP53* mutations predict clinical responses to decitabine in AML and MDS patients

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Supplemental Methods

Patient enrollment criteria

Inclusion:

All of the following:

1. Patient must have an ECOG performance status \leq 2.
2. Patient must have $>10\%$ disease burden measured by cytomorphology, flow cytometry, or cytogenetics.
3. Patient must have peripheral white blood cell count \leq 50,000/mcl.
4. Patient must have adequate organ function, defined as:
 - a. Total bilirubin \leq 1.5 x upper limit of normal
 - b. Aspartate aminotransferase and alanine aminotransferase \leq 2.5 x upper limit of normal.
 - c. Serum creatinine \leq 2.0 x upper limit of normal.
5. Patient must have undergone \leq 2 cycles of prior hypomethylating agent (decitabine or azacitidine).
6. Patient must be enrolled in HRPO# 201011766 (“Tissue Acquisition for Analysis of Genetic Progression Factors in Hematologic Diseases”).
7. Patient must be \geq 18 years of age.
8. Patient must be able to understand and willing to sign an IRB-approved written informed consent document.

Exclusion:

1. Patient must not be pregnant or nursing.
2. Patient must not have known CNS leukemia.
3. Patient must not have a history of positive HIV serology.

4. Patient must not have a history of positive Hepatitis C serology.
5. Patient must not have undergone a prior allogeneic stem cell transplant.
6. Patient must not have any uncontrolled intercurrent illness including, but not limited to, ongoing or active infection, ongoing or active GVHD, congestive heart failure of NYHA class 3 or 4, unstable angina pectoris, cardiac arrhythmia, or psychiatric illness/social situation that would limit compliance with study requirements.
7. Patient must not have had radiation therapy within 14 days of enrollment.
8. Patient must not have received any chemotherapy within 21 days of enrollment, and any acute treatment-related toxicities must have returned to baseline. Patients may be receiving hydrea at time of enrollment and may continue on hydrea through Cycle 2 of decitabine. An indication for hydrea following 2 cycles of decitabine is evidence that the patient is not responding and decitabine should be discontinued. Other than decitabine, patients cannot receive chemotherapy during this trial.

Statistical analysis

Analysis was performed using Excel (Microsoft, Seattle, WA), GraphPad (Prism, La Jolla, CA), and SAS Version 9.3 for Windows (SAS Institute Inc., Cary, NC).

Detailed description of statistical methods

Methylation analysis. Statistical analyses of the methylation data were done with repeated-measures analysis of variance. The dependent variable was the mean proportion of methylated CpGs measured at day 0 and day 10. Independent variables were Time, Disease (AML or MDS), and Response Group (CR/CRI/mCR or PR/SD/PD). Three analyses were done: one with

Time and Disease, one with Time and Response Group, and one with Time and both Disease Group.

Response analysis. The relationships between response (CR/CRi/mCR vs PR/SD/PD/NA) and other variables were evaluated with univariate logistic-regression models, two-way tables, and Pearson chi-square statistics for categorical variables and with t-tests for numeric variables. In addition, age and number of cycles completed were categorized and evaluated as categorical variables. Different groupings were examined for multi-level categorical variables to see if some groupings had stronger relationships with response. Variables with p-values less than 0.10 were used as covariates in bivariate logistic regression models, modeling the probability that a participant achieved blast clearance (CR/CRi/mCR).

Results of univariate logistic regression and response

Covariate	Intercept	Estimate	p-value	OR (95% CI)
TP53	-0.36	4.12	0.006	61.55 (2.27 - >999.999)
SRSF2	0.43	-1.68	0.006	0.19 (0.06 - 0.62)
Performance Status	0.73	-0.73	0.02	0.48 (0.27 - 0.87)
Cycles Completed	-0.75	1.63	0.0002	5.10 (2.19 - 11.89)
Transplant	-0.20	0.73	0.09	2.07 (0.90 - 4.78)
Age Group				
Disease	0.51			
MDS vs AML		0.25	0.65	1.29 (0.44 - 3.75)
Relapsed AML vs AML		-1.69	0.0008	0.19 (0.07 - 0.49)
Cytogenetic Risk	-0.49	1.45	0.0009	4.28 (1.81 - 10.13)

These variables, except for *TP53*, were also used as covariates in a stepwise multivariate logistic regression. The p-value for a variable to enter into the model was set at 0.10, as was the p-value for the variable to stay in the model. *TP53* was evaluated after a model had been built from the other variables because the sample had no participants with *TP53* mutations who did not achieve blast clearance (PR/SD/PD/NA), a quirk that leads to computation difficulties.

TP53 was added to the model constructed in the absence of that covariate and a new model was estimated.

Results of stepwise multivariate logistic regression and response

Model	Covariate	Estimate	Standard Error	p-value	OR (95% CI)
without TP53	Performance Status	12.22	0.48	0.01	0.30 (0.12 - 0.76)
	Cycles Completed	1.55	0.61	0.01	4.69 (1.41 - 15.60)
	MDS	-0.48	0.81	0.55	0.62 (1.41 - 3.03)
	Relapsed AML	-3.01	0.80	0.0002	0.05 (0.01 - 0.24)
	SRSF2	-2.21	0.86	0.01	0.11 (0.02 - 0.59)
with TP53	Performance Status	-1.53	0.51	0.003	0.22 (0.80 - 0.59)
	MDS	-1.23	0.82	0.13	0.29 (0.06 - 1.45)
	Relapsed AML	-3.03	0.83	0.0002	0.05 (0.01 - 0.24)
	TP53	4.25	1.60	0.008	70.44 (3.08 - >999.999)

Survival analysis. The relationship of each categorical covariate, including categorical versions of age and WBC, with overall survival was evaluated with Kaplan-Meier plots and log-rank statistics and proportional hazards regression for the continuous variables WBC and age. Survival was measured from the time of enrollment to either death or time of censoring (3/17/2016). Categories were combined when the plots suggested that it was reasonable to do so. The numeric variables age and WBC count were categorized and examined in Kaplan-Meier analyses for evidence of a linear relationship with survival. Those variables with log-rank p-values less than 0.20 were included in a stepwise multivariate proportional hazards analysis. Variables required a p-value of less than 0.20 to enter the model and a p-value of less than 0.10 to stay in the model. All two-way interactions among the variables remaining in the model were evaluated and retained along with the component variables if the p-value was less than 0.05. The interactions between the variables in the multivariate model and the two gene variables, *TP53* and *SRSF2*, were added to the model to see if there were any significant effects. The proportional hazards assumption was tested for the final multivariate model.

Detailed description of statistical results

Methylation analysis. Analyses showed a Time effect in all three models, with methylation levels dropping from day 0 to day 10. There was no Time by Disease interaction ($p = 0.74$) or Time by Response Group interaction ($p = 0.13$) in the models, nor was there a difference in methylation level by Disease. There was a significant effect of Response Group, with the PR/SD/PD group having slightly higher methylation levels at both Day 0 (0.54 (SD=0.02) vs 0.53 (SD=0.02)) and Day 10 (0.47 (SD=0.03) vs 0.44 (SD=0.03)). In the model without Disease Group the p-value was 0.01 and in the model with Disease included it was 0.02. There was no interaction between Disease Group and Response. The significant Response effect without a Response by Time interaction indicates that the methylation levels for both the CR/CRi/mCR and PR/SD/PD groups dropped at the same rate, with the PR/SD/PD group both starting at a higher level at Day 0 and ending at a higher level at Day 10.

Response analysis. Variables having a significant relationship ($p < 0.05$) with response were the genes *TP53* and *SRSF2*, Performance Status (coded as 0 or 1 vs 2 or 3), number of decitabine cycles completed (coded as 1 or 2 vs 3 or more), Disease Group (MDS vs AML vs Relapsed AML), and Cytogenetic Risk (categorized as Good or Intermediate vs Adverse). Results are presented here as Odds Ratio (95% Confidence Interval.) The variables associated with increased probability of blast clearance (CR/CRi/mCR) were *TP53* (61.6 (2.27 - >999.999)), number of chemotherapy cycles completed (5.1 (2.2 – 11.9)), and Cytogenetic Risk (4.3 (1.8 – 10.1)). The variables associated with decreased probability of CR/CRi/mCR were *SRSF2* (0.2 (0.1 – 0.6)), Performance Status (0.5 (0.3 – 0.9)), and Disease Group (no difference between MDS and AML; Relapsed AML vs AML: 0.2 (0.1 – 0.5)). The stepwise multivariate logistic model included these variables with the addition of Transplant (2.1 (0.9 – 4.)) and the subtraction of *TP53*. The lack of any cases with *TP53* mutation prevented its inclusion in a stepwise model. It was added to the multivariate model built from the other variables when a

statistical option, not available in the stepwise regression, could be used (SAS PROC LOGISTIC option FIRTH.) The model built without *TP53* contained *SRSF2*, Performance Status, number of chemotherapy cycles, and Disease Group. All p-values were less than 0.05 and odds ratios were similar to the odds ratios in the univariate results, though generally attenuated. The addition of *TP53* to the model caused *SRSF2* and number of chemotherapy cycles to become non-significant and they were dropped from the model. The odds ratios and confidence intervals for the variables in the model were Performance Status (0.2 (0.1 – 0.6)), Disease Group (MDS vs AML 0.3 (0.1 – 1.5), Relapsed AML vs AML 0.05 (0.01 – 0.24)), and *TP53* (70.4 (3.1 - >999.000)). Although *TP53* is strongly associated with CR, the extremely wide confidence ratio means that the point estimate of the odds ratio is very unreliable; it could be very far away from 70.4.

Survival Analysis. Variables associated with increased survival were CR/CRI/mCR (better than PD/NA or PR/SD), Transplant, Disease (MDS better than the combined AML and Relapsed AML), younger age, Performance Status of 0 and 1 compared to 2 and 3, and lower WBC (entered as log10(WBC)). Cytogenetic risk, *TP53* mutation, and *SRSF2* mutation were not associated with survival. The significant variables were included in a stepwise multivariate proportional hazards model. All but Response and Age were significant. The two-way interactions among the variables in the model were evaluated; the interaction of WBC and Performance Status was significant, showing that WBC has no effect when Performance Status is 2 or 3 but lower WBC is associated with better survival when Performance Status is 0 or 1. *TP53*, though not related to survival by itself, was added to the multivariate model along with its two-interactions. A significant interaction of *TP53* and Disease group was found. *TP53* status has no effect in the AML+Relapsed AML group but *TP53* wild type is associated with better survival among the MDS patients, but there are only 11 MDS patients with *TP53* wild type. *SRSF2* was evaluated in the same manner as *TP53* but no significant effects were found.

Results of stepwise multivariate proportional hazards model of survival

Covariate	Estimate	Standard Error	p-value	Hazard Ratio (95% CI)
Transplant	-1.48	0.39	<0.001	0.23 (0.11 - 0.49)
Performance Status = 3 or 4	2.28	0.57	< 0.001	9.73 (3.17 - 29.88)
log WBC	1.41	0.39	<0.001	4.11 (1.91 - 8.82)
MDS	-3.10	1.10	0.005	0.05 (0.005 - 0.38)
TP53	-0.12	0.49	0.80	0.89 (0.34 - 2.29)
Performance Status = 3 or 4 *				
log WBC	-1.41	0.63	0.03	0.24 (0.07 - 0.84)
TP53 * MDS	3.06	1.25	0.01	21.40 (1.84 - 248.83)

Enhanced Exome Sequencing

Three small insert dual indexed Illumina libraries were constructed with the 250ng of genomic DNA and the KAPA HTP library prep kit (KAPA Biosystems, Wilmington, MA) on the SciClone NGS platform (Perkin Elmer, Waltham, MA) according to the manufacturer's recommendations for each sample. The samples were fragmented on the Covaris LE220 (Covaris, Woburn, MA) targeting 100-400bp. Fifteen libraries from the same patient (5 different time points) were pooled precapture and 5 µg of library was hybridized with the Nimblegen version 3 exome reagent (Roche Nimblegen, Madison, WI) that covers ~64 Mb of the human genome. In addition to the exome space, a custom probe set was added through a spike in procedure using 120 bp biotinylated oligo nucleotides (IDT Lockdown Probes, Integrated DNA Technologies Coralville, IA) targeting a set of 264 recurrently mutated genes (RMG) (see Supplemental Methods A.2.3 ¹). The additional probes were added at an equal molar equivalent to the probe concentration of the exome probes, thus representing the RMG regions in a similar quantity as the exome regions. The libraries were hybridized for 72 hours at 47°C followed by stringent

washing. Enriched ssDNA library fragments were amplified with KAPA HiFi HotStart polymerase and 200nM primers prior to sequencing. The concentration of each captured library pool was accurately determined through qPCR according to the manufacturer's protocol (KAPA Biosystems, Wilmington, MA) to produce cluster counts appropriate for the Illumina HiSeq2000 platform. One lane of sequence data with 2x101bp reads was generated per capture pool, which yielded ~6-8Gb of data per sample.

Recurrently Mutated Gene (RMG) 264 gene panel sequencing

Library generation, alignment, variant identification, and filtering were performed as above, but capture only included the enhanced probes.

Amplicon 8 gene panel sequencing

The AmpliSeq probe panel targets exons 1 and 4-10 of TP53, as well as the sites of common mutations in DNMT3A (R882), IDH1 (R132), U2AF1 (S34), IDH2 (R172 and R140), SRSF2 (P95), and ASXL1. It also targets 30 additional sites on chromosome 17 that can be used to measure loss of heterozygosity.

Using the Ion AmpliSeq™ Designer version 5.2 (www.ampliseq.com), a BED file of 50 targets was successfully submitted for primer design under the Standard DNA workflow. Primers were delivered pre-pooled at 2X concentration. In conjunction with the AmpliSeq™ Library Kit 2.0, 50ng of input DNA in 6 μ l was combined with 10 μ l of the 2X custom AmpliSeq™ primer pool and 4 μ l of the 5X Ion AmpliSeq™ HiFi Mix. All reactions were cycled: 99°C for 2 minutes followed by 20 cycles of 99°C for 15 seconds and 60°C for 4 minutes. After amplification, primer sequences were digested by adding 2 μ l of FuPa Reagent and cycling at 50°C for 10 minutes, 55°C for 10 minutes, and 60°C for 20 minutes. Adapters were ligated onto the samples through

the addition of 4 μ l of Switch Solution, 2 μ l of Ion Xpress Barcode adapter mix, and 2 μ l of DNA Ligase. Samples were purified using 45 μ l of Ampure XP beads (Agencourt/Beckman Coulter). The libraries were quantified through use of the KAPA Library Quantification Kit for Ion Torrent and diluted to 100pM with Ion Torrent Low TE. Dilutions of anywhere from 20-24 libraries were then pooled together. Template preparation was carried out on the Ion OneTouch 2 instrument in conjunction with the Ion Personal Genome Machine® (PGM™) Hi-Q OT2 Template Prep Kit according to revision A of the associated protocol (publication part number MAN0010902). The 400bp workflow was selected. The amplification reaction consisted of 25 μ l of nuclease-free water, 800 μ l of Ion PGM™ Hi-Q Reagent Mix, 50 μ l of Ion PGM™ Hi-Q Enzyme Mix, 25 μ l of the pooled library diluted to 8pM, and 100 μ l of Ion PGM™ HiQ Ion Sphere™ Particles (ISPs). Following automated template prep on the OneTouch™ 2, enrichment of template-positive ISPs was done on the Ion OneTouch™ ES instrument.

The Ion PGM Hi-Q Sequencing Kit was used for sequencing on the Ion Torrent PGM™ according to the revision D.0 of the manufacturer's protocol (publication part number MAN0009816). Each library pool was sequenced on a single Ion 318™ Chip Kit (v2) with 400bp read length settings (850 flows). Torrent Suite version 5.0.2 was used to provide preliminary coverage analysis against the custom target regions.

Sequence analysis

Sequence data were aligned to reference sequence build GRCh37-lite-build37 using bwa version 0.5.9² (parameters: -t = 4, -q = 5), then merged using picard version 1.46³, and deduplicated using picard version 1.46.

SNVs were detected using the union of three callers: (1) the output of samtools version r963³ (parameters: -A -B), intersected with the output of SomaticSniper version 1.0.2⁴ (parameters: -F vcf -q 1 -Q 15), and filtered through false-positive-filter v1 (parameters: --bam-readcount-version 0.4 --bam-readcount-min-base-quality 15 --min-mapping-quality 40 --min-somatic-score 40), (2) the output of VarScan version 2.2.6⁵, filtered using varscan-high-confidence filter version v1 and false-positive filter v1 (parameters: --bam-readcount-version 0.4 --bam-readcount-min-base-quality 15), and (3) Strelka version 0.4.6.2⁶ (parameters: isSkipDepthFilters = 1).

Indels were detected using the union of 4 callers: (1) GATK somatic-indel version 5336⁷, filtered using false-indel version v1 (params: --bam-readcount-version 0.4 --bam-readcount-min-base-quality 15), (2) pindel version 0.5⁸, filtered with pindel-somatic-calls v1, pindel-vaf-filter v1 (params: --variant-freq-cutoff=0.08), and pindel-read-support v1, (3) VarScan version 2.2.6⁵, filtered with varscan-high-confidence-indel version v1, then with false-indel version v1 (parameters: --bam-readcount-version 0.4 --bam-readcount-min-base-quality 15), and (4) Strelka version 0.4.6.2⁶ (parameters: isSkipDepthFilters = 1).

Variants were subsequently filtered to exclude those that are frequently identified in normal (non-tumor) samples from a large set of in-house sequencing data, are non-genic with a tumor VAF below 20%, score below noise in a binomial test (LLR threshold = 5), have an EVS allele frequency below 0.1, or failed manual review of aligned sequence data (with the exception of known AML hotspot mutations, listed in eTable 18,¹ which were included even if they failed manual review).

To be included in the final time course data set for a given patient, variants were required to be present significantly above noise at one or more time points ($p \leq 0.05$, Fisher Exact test), to

have at least 50-fold coverage in the normal sample, and to have at least 50-fold coverage averaged across the tumor samples.

Copy number analysis was performed using VarScan2⁵.

Analysis of mutation spectrum. A two-sided Fisher's exact test was used to show that the frequency of transversions is significantly higher after decitabine treatment than before ($p = 6 \times 10^{-9}$). This is attributable to an increase in C-to-G ($p = 6 \times 10^{-7}$) and G-to-C ($p = 6 \times 10^{-11}$) transversions after decitabine exposure. In these analyses, mutations were pooled across all patients for whom we had collected samples at or later than the second cycle of decitabine treatment. A mutation was counted as a "Day 0" mutation if it was detectable at Day 0; it was counted as a post-decitabine mutation if it was detectable only at or later than the second cycle of treatment. These results are similar to the results previously observed by Jackson-Grusby, et al.⁹

Illumina 450k methylation arrays

Genomic DNA (250-500ng per sample) was bisulfite-converted, amplified, fragmented, precipitated, hybridized to Illumina Infinium 12-sample BeadChips, and scanned using an iScan System according to the Infinium HD Methylation Assay Guide (Illumina document 15019519 v01). Subsequent analyses were performed using R3.0.2. First, the data was filtered based on detection p -value and beadcount, using the pfilter function of the wateRmelon R package (default parameters), and probes corresponding to the X and Y chromosomes were removed. Background correction was performed using the "noob" function from the methylumi package. The BMIQ function from the wateRmelon package was used to correct for type-II probe bias. Color bias was removed using the lumiMethyC function from the lumi package. Finally, the data

was filtered to include only those probes for which we had complete data across all samples (473,606 probes).

LC/MS/MS analysis of decitabine

Peripheral blood (3ml) was collected on day 4 ± 1 in EDTA tubes with 4 mcg tetrahydrouridine. Samples were collected 45 minutes ± 15 minutes after beginning the infusion to assure steady state pharmacokinetics, and stored as plasma.¹⁰

Decitabine was extracted from human plasma by acetonitrile extraction. Plasma (100 µL) was mixed with 400 µL of acetonitrile and 20 ng of nitrogen-15 labeled commercial decitabine-¹⁵N₄ as the internal standard (please fill in the commercial source), vortexed several times, centrifuged at 4 °C for 5 minutes. The supernatant was dried under a stream of nitrogen and was re-dissolved in 500 µL of 0.1 % formic acid in water. Five point calibration samples (5ng, 10 ng, 20ng, 50ng, and 500ng in 500 µL of 0.1 % formic acid in water) of commercial decitabine (Sigma-Aldrich, St. Louis, MO) containing the internal standard (20 ng) were also prepared for the absolute quantification. 20 µL of the plasma extracts as well as the calibration samples was injected onto a C18 column (Phenomenex Kinetic, 100x3.0 mm, 3 µm, Torrance, CA) connected to a Shimadzu 20AD HPLC system (Kyoto, Japan), interfaced with an API-4000 triple quadruple mass spectrometer (Applied Biosystems, Foster City, CA) for decitabine analysis. Acetonitrile containing 0.1 % formic acid (B) and water containing 0.1 %formic acid (A) were used for LC/MS/MS of decitabine and the internal standard. The solvent gradient was at 3% B at the beginning and was then programmed to 30% B for 2.5 min at a flow rate of 0.7 ml/min. Positive ion electrospray MRM mode (monitoring Q1/Q3 ions: 229/113 for decitabine and 233/117 for decitabine-¹⁵N₄, Toronto Research Chemicals, Toronto, Ontario) was controlled by Analyst software (Applied Biosystems) for quantification of decitabine.

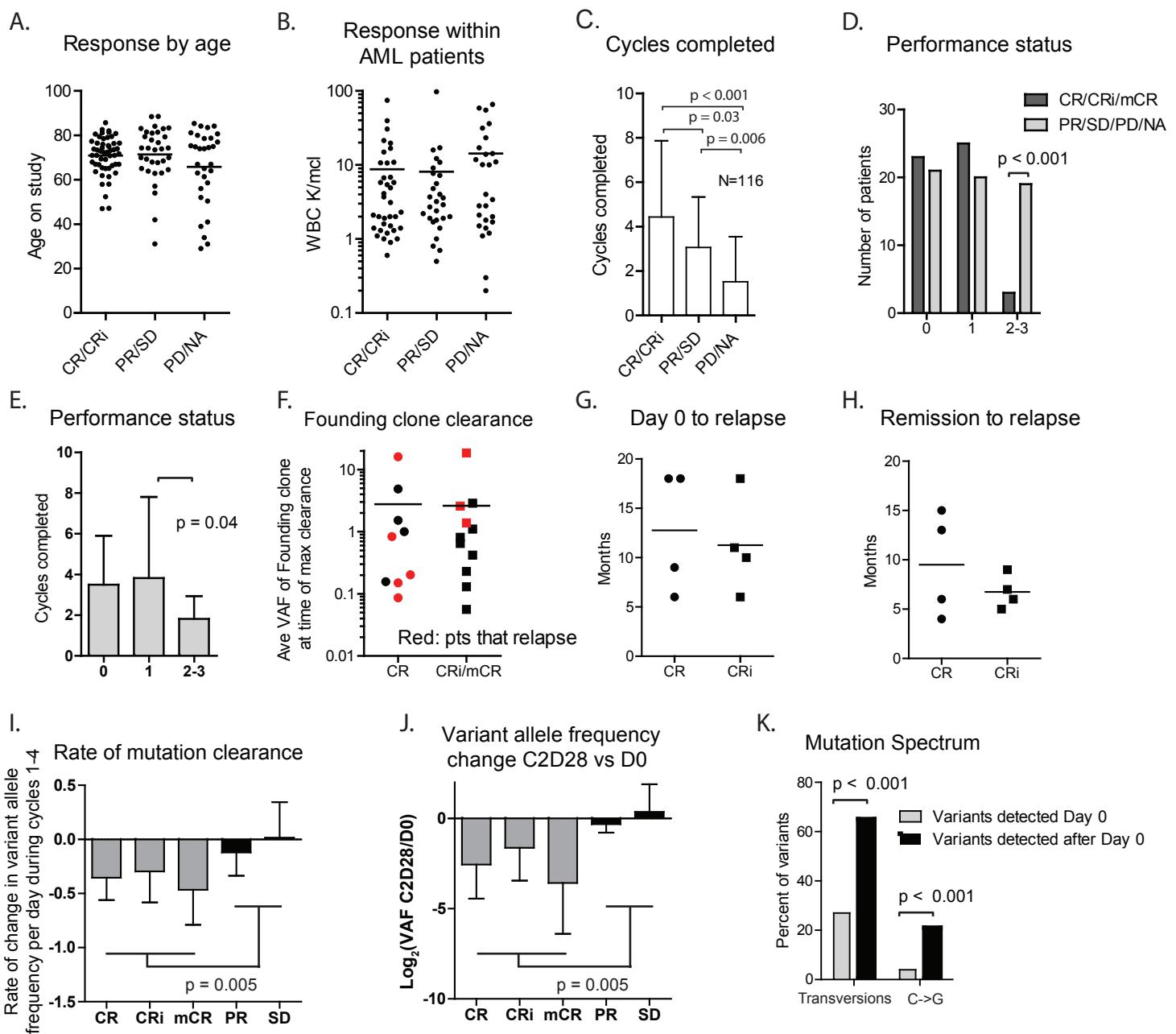


Figure S1. Clinical parameters and relationships with outcomes. A. Comparison of patient age at time of enrollment and morphologic response. B. Comparison of white blood cell count (WBC) at time of enrollment and morphologic response. C. Comparison of the number of cycles of decitabine received and morphologic response. D. Comparison of performance status at time of enrollment and morphologic response. E. Comparison of performance status and the number of cycles of decitabine received. F. Average variant allele frequency (VAF) of founding clone mutations during remission in patients with morphologic CR vs. CRI/mCR. G. Time from start of cycle 1 of decitabine to relapse in the 8 patients indicated in black in F. H. Time from first morphologic remission until relapse in the 8 patients indicated in black in F. I. Rate of mutation clearance in 54 cases evaluated at a median of 4 time points per case. J. VAF change observed in 44 cases evaluated on Day 0 and C2D28. P values calculated with one way ANOVA and Tukey's multiple comparison test. Similar statistical results were obtained for the parameters in A-E using a univariate logistic regression model. In that model, response correlated with the presence of TP53 mutations ($p = 0.006$), the absence of SRSF2 mutations ($p = 0.006$), performance status 0/1 vs 2/3 ($p < 0.02$), three or more cycles completed ($p = 0.0002$), untreated AML or MDS vs relapsed AML ($p < 0.001$), adverse risk cytogenetics vs. intermediate/good risk cytogenetics ($p < 0.0009$). In multivariate step-wise regression, only TP53 ($p = 0.008$, odds ratio 70.44: 95% CI 3.08 -> 999), performance status 2/3 ($p = 0.003$, odds ratio 0.22: 95% CI 0.8 - 0.59), and relapsed AML ($p < 0.001$, odds ratio 0.05: 95% CI 0.01-0.24) were significant determinants of clinical response (see Supplemental Methods). K. Mutation spectrum in diagnostic samples vs. variants that emerge following decitabine, demonstrated a shift toward C->G transversions.

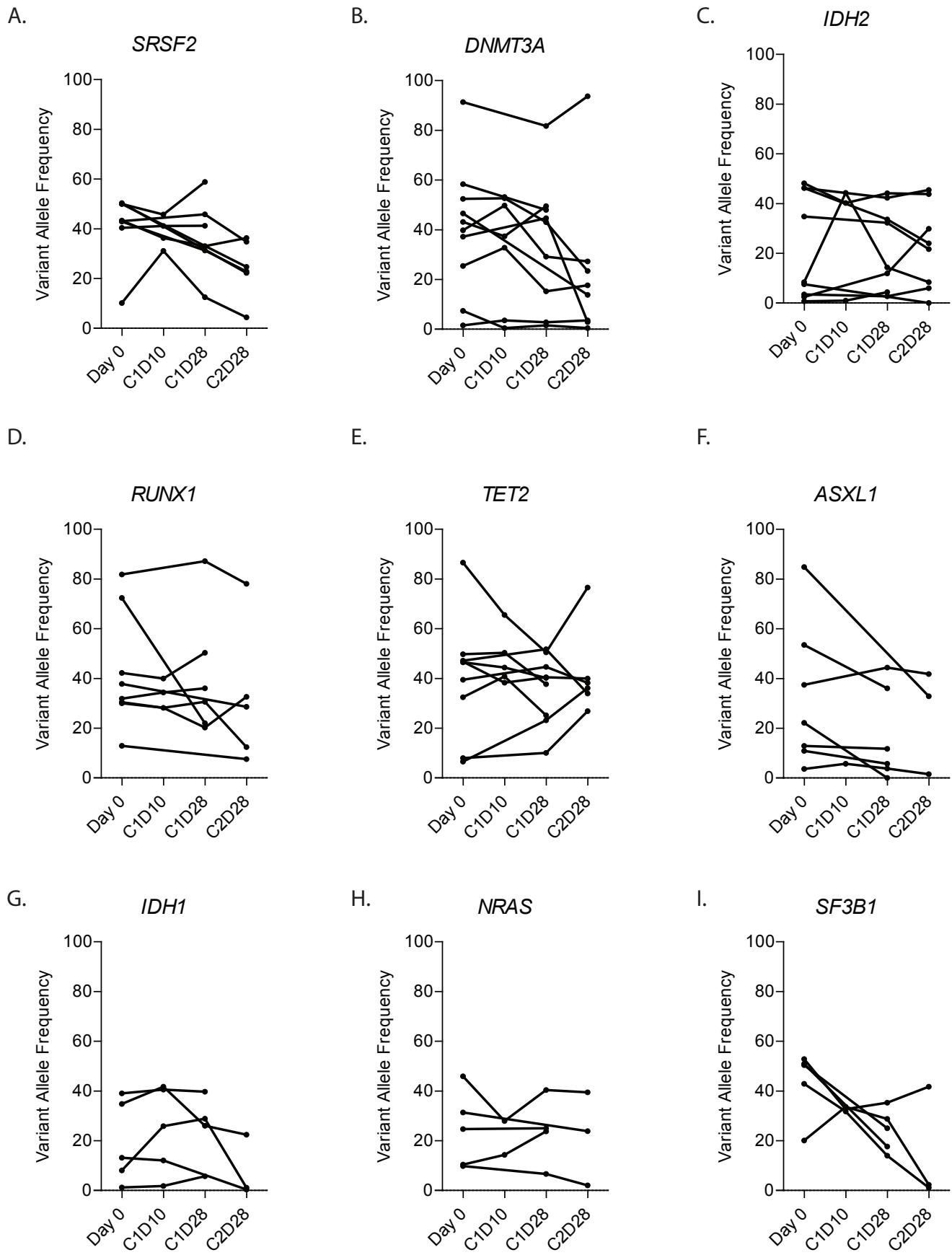
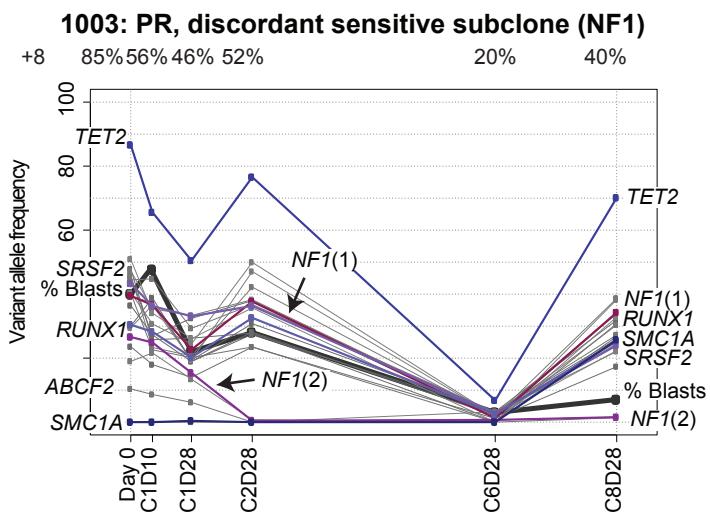
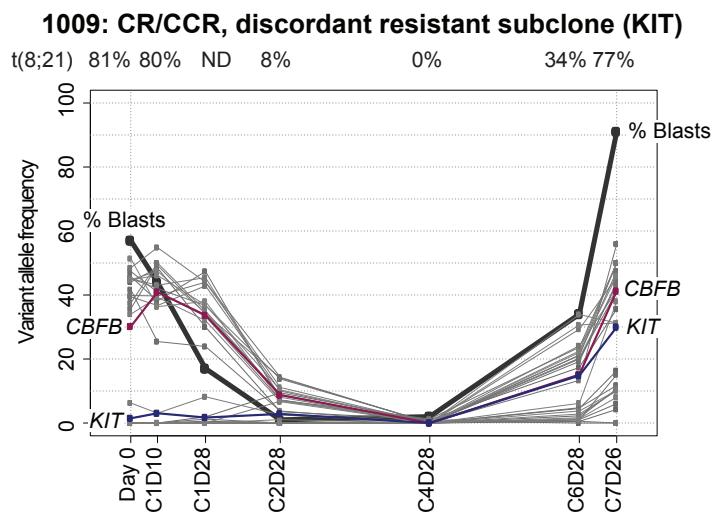


Figure S2. Rate of mutation reduction. A – I. Representative data for mutations occurring in individual genes.

A.



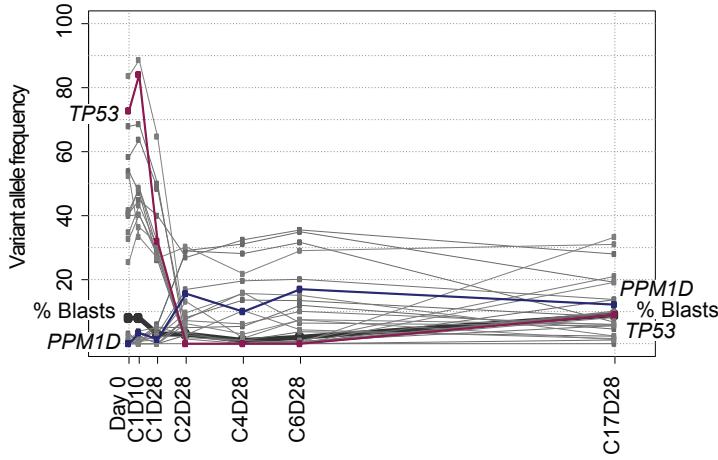
B.



C.

1014: CR/CCR, unrelated clonal hematopoiesis

Del5q 74% 48% 3% 0% 0% 44%



D.

1036: CRi/CCR, persistant founding clone

+8 35% 32% 0% 0%

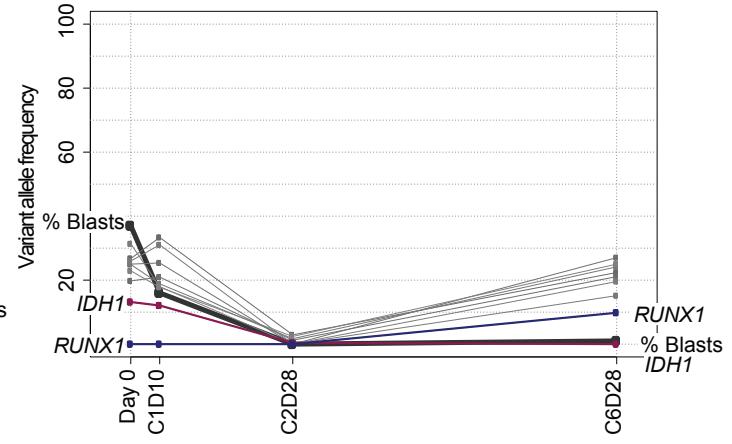


Figure S3. Representative discordant response in subclones. The variant allele frequency (VAF) is indicated on the Y-axis. Time is indicated on the X-axis (C1D10 = cycle 1 day 10, etc). Mutations in genes that are recurrently mutated in AML/MDS are highlighted in blue and red. Morphologic blast counts are indicated in bold black. Clinical cytogenetics and responses are indicated above each plot. Patient specific “private” mutations are indicated in grey.

A. Patient 1003. This patient carries biallelic NF1 mutations. Note the second NF1 mutation (2) and the ABCF2 mutation both undergo near complete clearance by the end of cycle 2 (C2D28), whereas the VAFs of founding clone mutations (SRSF2, NF1(1), and RUNX1) largely are unchanged, suggesting subclonal sensitivity within a background of a resistant founding clone. Note that even though the NF1(2) subclone is robustly reduced by C2D28, it is not completely cleared, and the NF1(2) mutation is again detectable at relapse (C8D28). Note that a subclone containing an SMC1A mutation, which was not detectable at diagnosis (Day 0) expands and drives the relapse (C8D28).

B. Patient 1009. Note the marked reduction in the founding clone VAFs (CBFB) by the end of cycle 2 (C2D28), whereas the subclone KIT mutation is unchanged, suggesting intrinsic decitabine resistance in an otherwise decitabine sensitive background. Note the KIT subclone expands and gives rise to the relapse. The patient completed decitabine dosing in cycle 7 before the pathology report noted relapse at the end of cycle 6 (C6D28), and a repeat bone marrow biopsy was obtained at the end of cycle 7 before the patient transitioned to alternative chemotherapy. Note that the relapse clone continued to expand during cycle 7, further suggesting decitabine resistance.

C. Patient 1014. Note that during remission there is expansion of “rising clones” that are unrelated to the TP53 founding clone, but instead contain a PPM1D mutation and other private mutations.

D. Patient 1036. Note the clearance of the IDH1 mutation in the founding clone, but expansion of a “rising clone” during remission that contains private founding clone mutations and a new RUNX1 mutation.

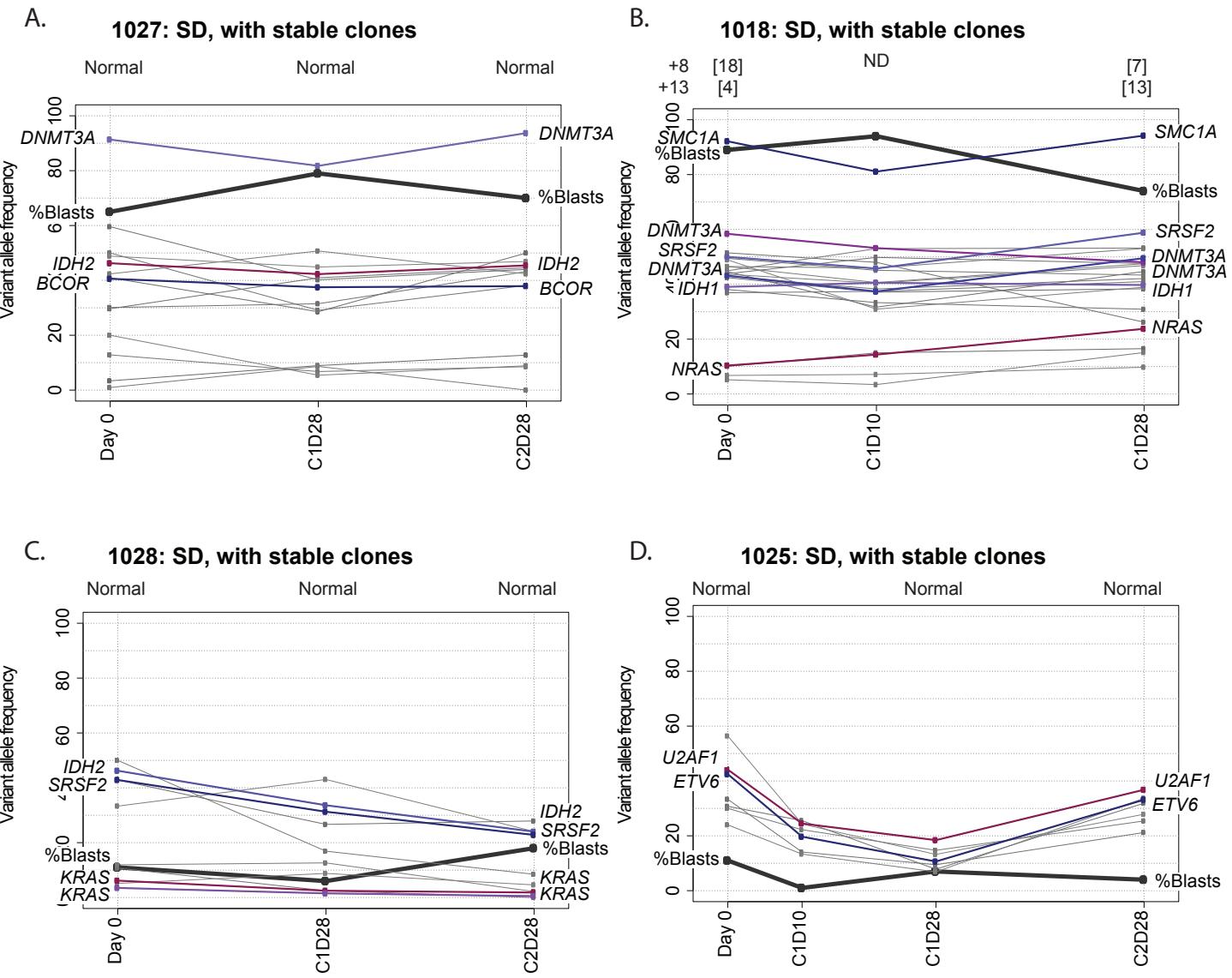


Figure S4. Representative cases with stable disease (SD). Note that mutation variant allele frequencies are relatively constant across multiple bone marrow samples during morphologic stable disease.

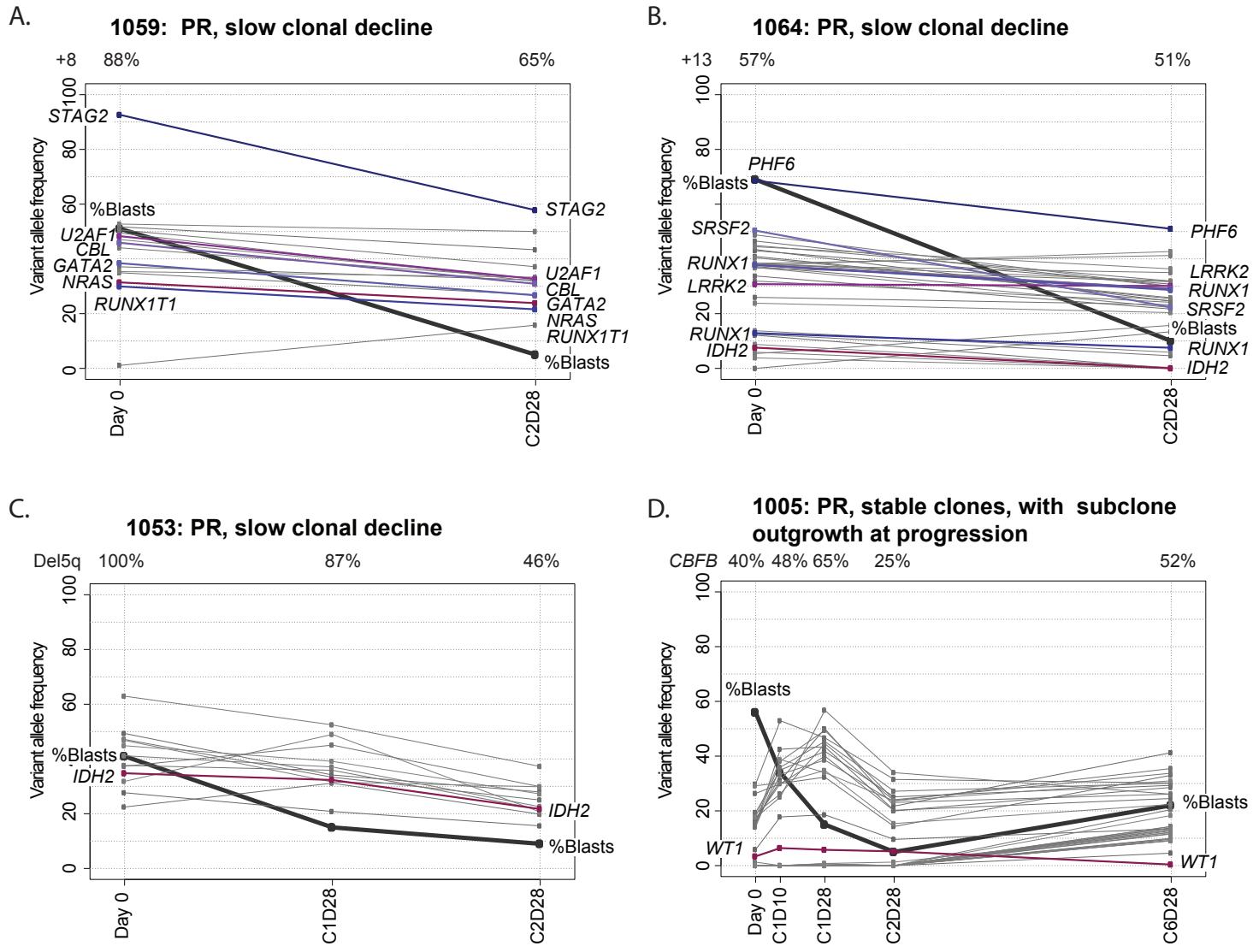


Figure S5. Representative cases with partial response (PR). Note that in cases with partial response, variant allele frequency reduction is slow, and often preceded by blast clearance.

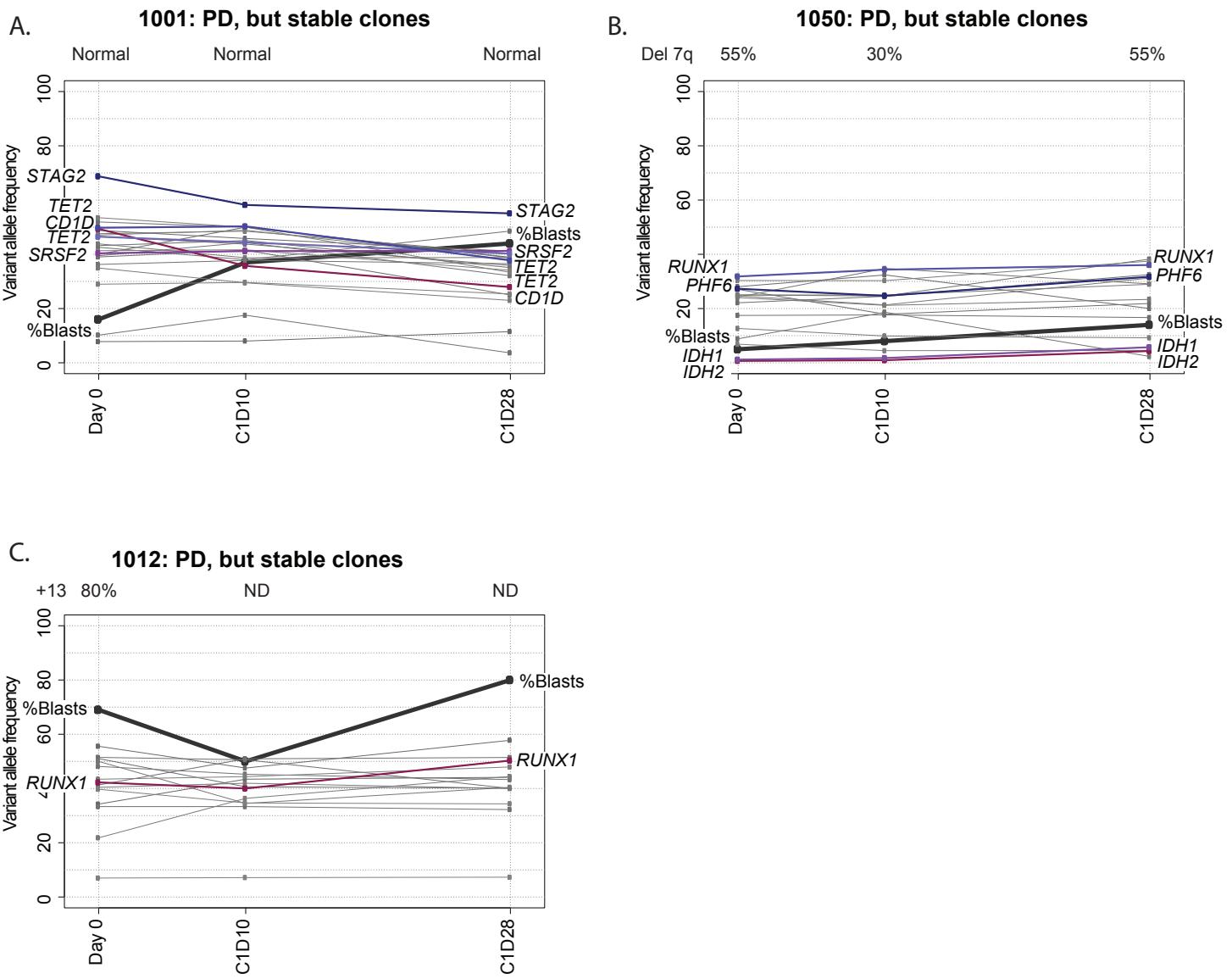
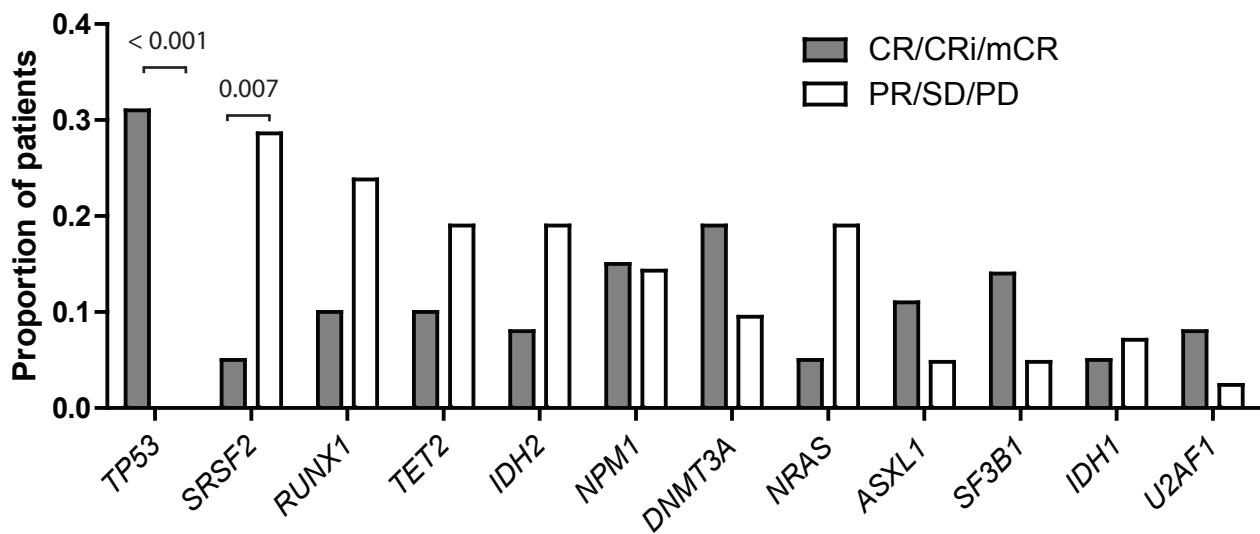


Figure S6. Cases with progressive disease (PD). Note that variant allele frequencies remain relatively constant even though patients are clinically progressing. Progression was determined by blast counts (A and B), and by WBC and LDH (C).

A.

AML

B.

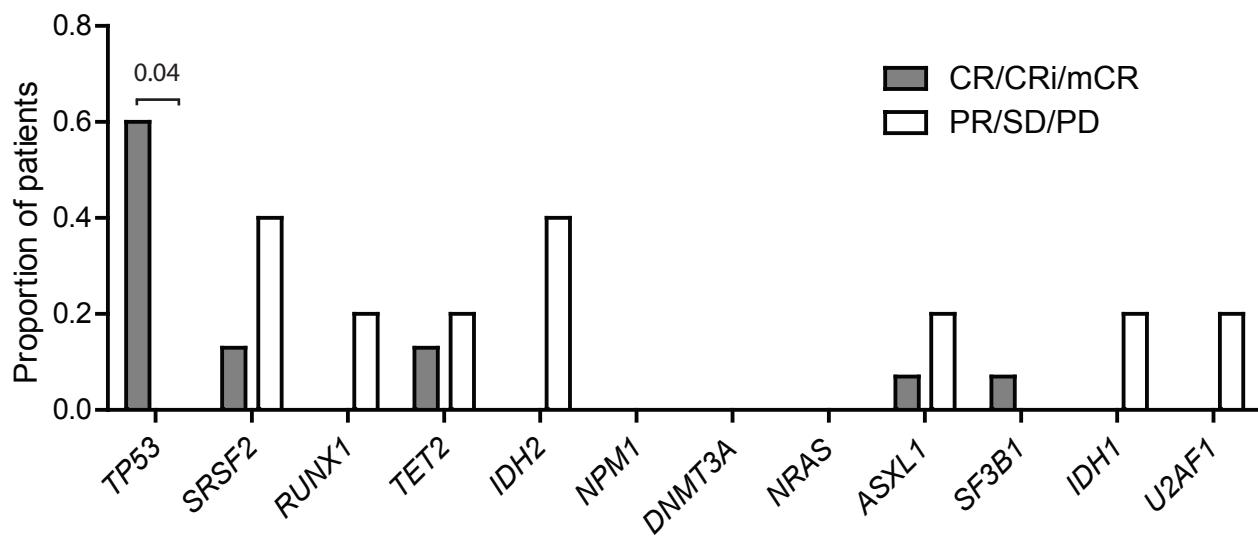
MDS

Figure S7. Comparison of the proportion of responding and non-responding patients with AML or MDS with indicated mutations. A. Patients with AML. B. Patients with MDS. P values represent results from Fisher exact test, when significant.

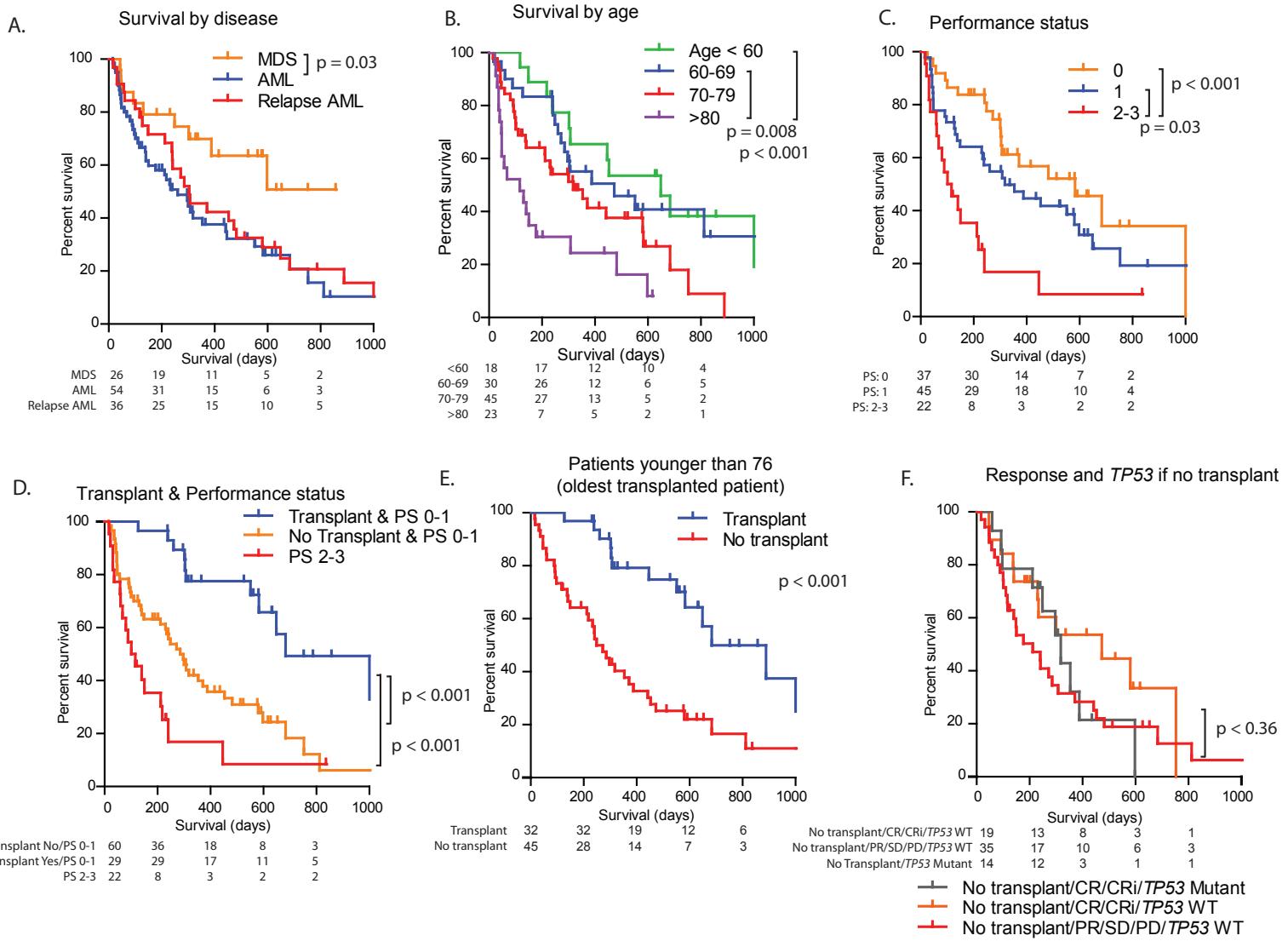
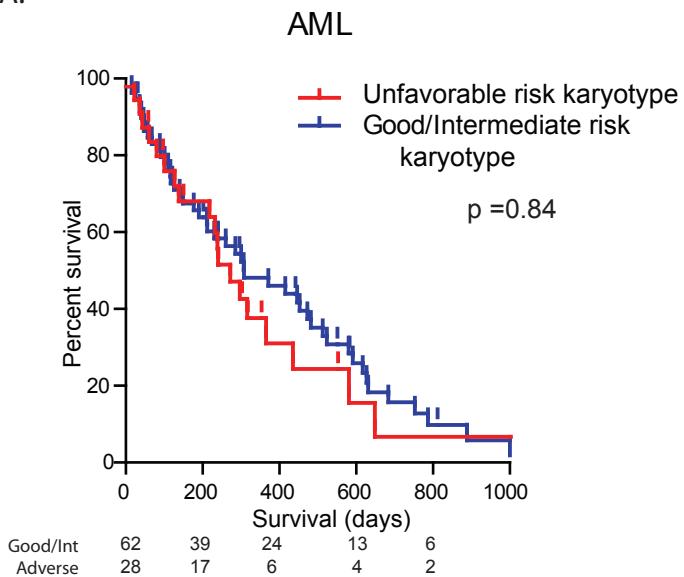
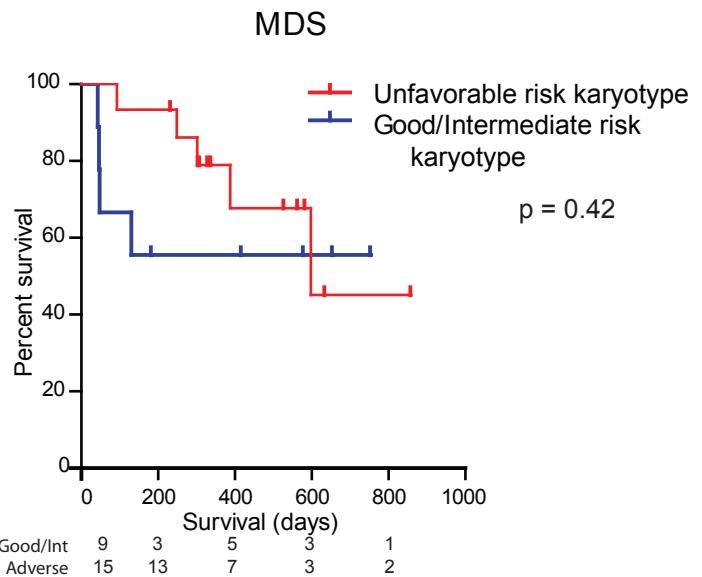


Figure S8. Subgroup survival analysis. A. Overall survival correlated with disease status in patients with MDS, AML, and relapsed AML. B. Overall survival correlated with decade of life at time of enrollment. C. Overall survival correlated with performance status 0, 1, or 2 and 3. Note that only one patient in the cohort had a performance status of 3, and that performance status data was not available for 12 patients. D. Overall survival among patients with performance status 0 and 1 correlated with transplant status. Note that only 2 patients with performance status of 2 or 3 underwent stem cell transplantation. E. Overall survival in patients younger than 76 (the oldest patient transplanted was 76). F. Overall survival in non-transplanted patients based on TP53 status and responses. Despite a significant improvement in the rate of complete response among patients with a TP53 mutation, and a correlation between response and overall survival for the entire cohort, there was no significant difference in overall survival based on TP53 mutation status. Nearly two thirds of responding cases did not have complete count recovery, and were exposed to the complications of prolonged cytopenias. Without progression to transplantation, the survival benefit of response is largely mitigated. P values represent results from Log-rank test, when comparing two factors, and pair-wise log rank analysis, when comparing more than two. Similar results were obtained in a stepwise Cox proportional hazards model of overall survival.

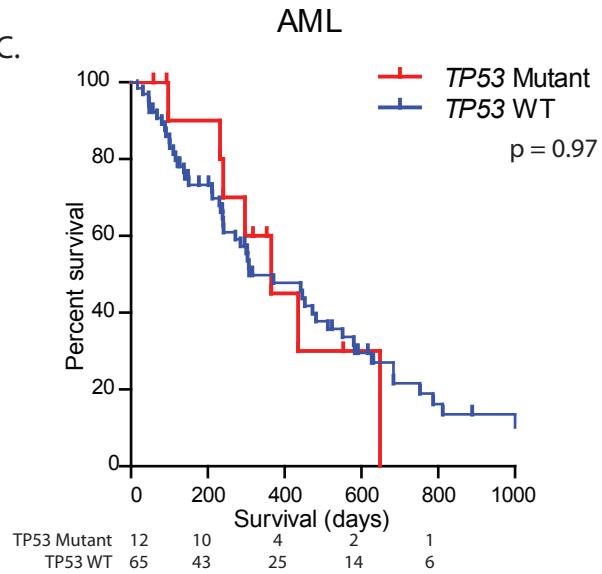
A.



B



C.



D.

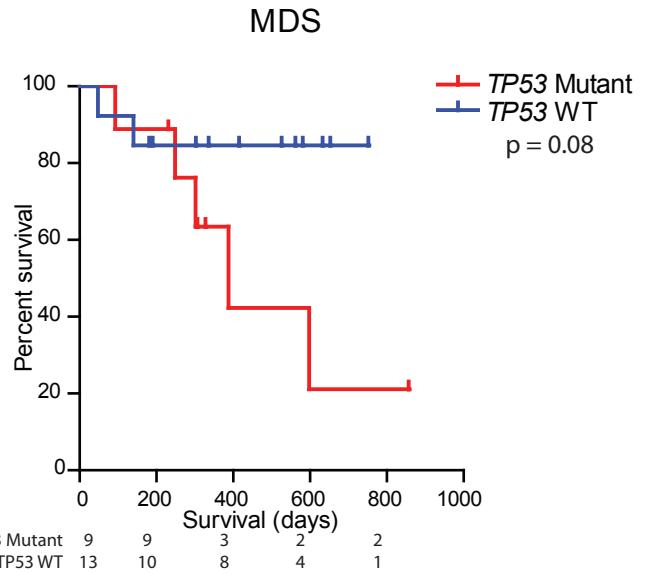


Figure S9. Subgroup survival analysis, AML vs. MDS patients. A and C. Overall survival in AML patients with adverse risk karyotype (A) or TP53 mutation (C). B and D. Overall survival in MDS patients with adverse risk karyotype (B) or TP53 mutation (D). P values represent results from Log-rank test.

Table S1. Coverage summary

Case	Sample	Time	Technique	Average reads/nucleotide
322879	normal	Day0	RMG	405
322879	tumor	Day0	RMG	392
371766	normal	Day0	RMG	351
371766	tumor	Day0	RMG	457
505186	normal	Day0	RMG	371
505186	tumor	Day0	RMG	381
654840	normal	Day0	RMG	401
654840	tumor	Day0	RMG	404
692847	normal	Day0	RMG	389
692847	tumor	Day0	RMG	474
790809	normal	Day0	RMG	412
790809	tumor	Day0	RMG	416
800684	normal	Day0	RMG	396
800684	tumor	Day0	RMG	404
1001	tumor	C1D10	Enhanced exome	69
1001	tumor	C1D28	Enhanced exome	71
1001	normal	Day0	Enhanced exome	56
1001	tumor	Day0	Enhanced exome	59
1002	tumor	C1D10	Enhanced exome	73
1002	tumor	C1D28	Enhanced exome	55
1002	tumor	C2D28	Enhanced exome	54
1002	normal	Day0	Enhanced exome	58
1002	tumor	Day0	Enhanced exome	56
1003	normal	C1D10	Enhanced exome	62
1003	tumor	C1D10	Enhanced exome	60
1003	tumor	C1D28	Enhanced exome	61
1003	tumor	C2D28	Enhanced exome	68
1003	tumor	C6D28	Enhanced exome	48
1003	tumor	C8D28	Enhanced exome	65
1003	tumor	Day0	Enhanced exome	57
1004	tumor	C1D10	Enhanced exome	58
1004	tumor	C1D28	Enhanced exome	53
1004	tumor	C2D28	Enhanced exome	63
1004	tumor	C4D28	Enhanced exome	55
1004	normal	C6D28	Enhanced exome	41
1004	tumor	C6D28	Enhanced exome	68
1004	tumor	C8D28	Enhanced exome	60

1004	tumor	Day0	Enhanced exome	61
1005	tumor	C1D28	Enhanced exome	71
1005	normal	C2D28	Enhanced exome	56
1005	tumor	C2D28	Enhanced exome	57
1005	tumor	C6D28	Enhanced exome	76
1005	tumor	Day0	Enhanced exome	55
1005	tumor	Day10	Enhanced exome	61
1008	tumor	C1D10	Enhanced exome	65
1008	tumor	C1D28	Enhanced exome	62
1008	tumor	C2D28	Enhanced exome	69
1008	normal	Day0	Enhanced exome	55
1008	tumor	Day0	Enhanced exome	62
1009	tumor	C1D10	Enhanced exome	65
1009	tumor	C1D28	Enhanced exome	70
1009	tumor	C2D28	Enhanced exome	65
1009	tumor	C4D28	Enhanced exome	85
1009	tumor	C6D28	Enhanced exome	74
1009	tumor	C6D57	Enhanced exome	58
1009	tumor	C7D26	Enhanced exome	76
1009	normal	Day0	Enhanced exome	61
1009	tumor	Day0	Enhanced exome	47
1010	tumor	C16	Enhanced exome	74
1010	tumor	C17	Enhanced exome	71
1010	tumor	C1D10	Enhanced exome	46
1010	tumor	C1D28	Enhanced exome	52
1010	tumor	C2D28	Enhanced exome	44
1010	tumor	C4D28	Enhanced exome	68
1010	tumor	C6D28	Enhanced exome	39
1010	normal	C8D28	Enhanced exome	41
1010	tumor	C8D28	Enhanced exome	160
1010	tumor	Day0	Enhanced exome	51
1011	tumor	C1D10	Enhanced exome	67
1011	tumor	C1D28	Enhanced exome	67
1011	normal	C2D28	Enhanced exome	59
1011	tumor	C2D28	Enhanced exome	65
1011	tumor	Day0	Enhanced exome	62
1012	tumor	C1D10	Enhanced exome	64
1012	normal	C1D28	Enhanced exome	57
1012	tumor	C1D28	Enhanced exome	64
1012	tumor	Day0	Enhanced exome	51
1013	normal	Day0	RMG	357

1013	tumor	Day0	RMG	365
1014	tumor	C17	Enhanced exome	48
1014	tumor	C1D10	Enhanced exome	63
1014	tumor	C1D28	Enhanced exome	68
1014	tumor	C2D28	Enhanced exome	72
1014	normal	C4D28	Enhanced exome	61
1014	tumor	C4D28	Enhanced exome	61
1014	tumor	C6D28	Enhanced exome	131
1014	tumor	Day0	Enhanced exome	58
1016	tumor	C1D10	Enhanced exome	66
1016	normal	C1D28	Enhanced exome	57
1016	tumor	C1D28	Enhanced exome	71
1016	tumor	C2D28	Enhanced exome	65
1016	tumor	Day0	Enhanced exome	67
1017	tumor	C10D2	Enhanced exome	69
1017	tumor	C1D10	Enhanced exome	58
1017	normal	C2D28	Enhanced exome	59
1017	tumor	C2D28	Enhanced exome	71
1017	tumor	C6D28	Enhanced exome	72
1017	tumor	Day0	Enhanced exome	66
1018	normal	C1D10	Enhanced exome	46
1018	tumor	C1D10	Enhanced exome	65
1018	tumor	C1D28	Enhanced exome	65
1018	tumor	Day0	Enhanced exome	64
1019	tumor	C1D10	Enhanced exome	67
1019	tumor	C1D28	Enhanced exome	68
1019	tumor	C2D28	Enhanced exome	66
1019	normal	C3D28	Enhanced exome	56
1019	tumor	C3D28	Enhanced exome	73
1019	tumor	Day0	Enhanced exome	65
1021	tumor	C1D10	Enhanced exome	64
1021	tumor	C1D28	Enhanced exome	55
1021	tumor	C2D28	Enhanced exome	59
1021	tumor	C6	Enhanced exome	42
1021	normal	Day0	Enhanced exome	52
1021	tumor	Day0	Enhanced exome	61
1022	tumor	C1D10	Enhanced exome	59
1022	normal	C1D28	Enhanced exome	144
1022	tumor	C1D28	Enhanced exome	31
1022	tumor	C2D28	Enhanced exome	47
1022	tumor	Day0	Enhanced exome	48

1023	normal	C1D10	Enhanced exome	54
1023	tumor	C1D10	Enhanced exome	66
1023	tumor	C1D28	Enhanced exome	61
1023	tumor	C2D28	Enhanced exome	65
1023	tumor	C4D28	Enhanced exome	68
1023	tumor	C6D28	Enhanced exome	73
1023	tumor	C8D28	Enhanced exome	69
1023	tumor	Day0	Enhanced exome	55
1024	tumor	C1D10	Enhanced exome	58
1024	tumor	C1D28	Enhanced exome	48
1024	normal	Day0	Enhanced exome	47
1024	tumor	Day0	Enhanced exome	51
1025	tumor	C1D10	Enhanced exome	74
1025	tumor	C1D28	Enhanced exome	76
1025	tumor	C2D28	Enhanced exome	73
1025	normal	Day0	Enhanced exome	53
1025	tumor	Day0	Enhanced exome	55
1027	tumor	C1D28	Enhanced exome	78
1027	normal	C2D28	Enhanced exome	51
1027	tumor	C2D28	Enhanced exome	68
1027	tumor	Day0	Enhanced exome	66
1028	normal	C1D28	Enhanced exome	62
1028	tumor	C1D28	Enhanced exome	79
1028	tumor	C2D28	Enhanced exome	62
1028	tumor	Day0	Enhanced exome	73
1029	normal	Day0	Enhanced exome	55
1029	tumor	Day0	Enhanced exome	60
1029	tumor	PreSt	Enhanced exome	70
1035	tumor	C1D10	Enhanced exome	52
1035	tumor	C1D28	Enhanced exome	63
1035	normal	C2D28	Enhanced exome	43
1035	tumor	C2D28	Enhanced exome	62
1035	tumor	C2D31	Enhanced exome	70
1035	tumor	Day0	Enhanced exome	65
1036	tumor	C1D10	Enhanced exome	75
1036	tumor	C2D28	Enhanced exome	72
1036	tumor	C6D28	Enhanced exome	62
1036	normal	Day0	Enhanced exome	56
1036	tumor	Day0	Enhanced exome	76
1037	normal	Day0	RMG	278

1037	tumor	Day0	RMG	496
1038	normal	Day0	RMG	310
1038	tumor	Day0	RMG	461
1040	tumor	C1D28	Enhanced exome	55
1040	tumor	C2D28	Enhanced exome	53
1040	normal	Day0	Enhanced exome	43
1040	tumor	Day0	Enhanced exome	49
1041	tumor	C1D28	Enhanced exome	41
1041	tumor	C2D28	Enhanced exome	44
1041	tumor	C5D42	Enhanced exome	62
1041	normal	Day0	Enhanced exome	30
1041	tumor	Day0	Enhanced exome	41
1042	normal	C2D28	Enhanced exome	50
1042	tumor	C2D28	Enhanced exome	67
1042	tumor	Day0	Enhanced exome	65
1043	normal	C1D28	Enhanced exome	48
1043	tumor	C1D28	Enhanced exome	63
1043	tumor	C2D28	Enhanced exome	55
1043	tumor	Day0	Enhanced exome	57
1044	normal	C1D28	Enhanced exome	54
1044	tumor	C1D28	Enhanced exome	63
1044	tumor	Day0	Enhanced exome	72
1045	tumor	C1D28	Enhanced exome	68
1045	tumor	C2D28	Enhanced exome	68
1045	tumor	C4D73	Enhanced exome	69
1045	normal	Day0	Enhanced exome	58
1045	tumor	Day0	Enhanced exome	77
1047	normal	Day0	RMG	284
1047	tumor	Day0	RMG	396
1048	normal	Day0	RMG	344
1048	tumor	Day0	RMG	422
1049	tumor	C1D10	Enhanced exome	72
1049	normal	C1D28	Enhanced exome	61
1049	tumor	C1D28	Enhanced exome	76
1049	tumor	C2D28	Enhanced exome	73
1049	tumor	Day0	Enhanced exome	73
1050	normal	C1D10	Enhanced exome	57
1050	tumor	C1D10	Enhanced exome	76
1050	tumor	C1D28	Enhanced exome	74
1050	tumor	Day0	Enhanced exome	77
1051	tumor	C1D28	Enhanced exome	74

1051	tumor	C2D28	Enhanced exome	66
1051	normal	Day0	Enhanced exome	58
1051	tumor	Day0	Enhanced exome	68
1053	normal	C1D28	Enhanced exome	49
1053	tumor	C1D28	Enhanced exome	67
1053	tumor	C2D28	Enhanced exome	75
1053	tumor	Day0	Enhanced exome	68
1055	tumor	C1D28	Enhanced exome	65
1055	normal	Day0	Enhanced exome	69
1055	tumor	Day0	Enhanced exome	67
1057	normal	Day0	RMG	378
1057	tumor	Day0	RMG	394
1058	tumor	C1D28	Enhanced exome	64
1058	tumor	C2D28	Enhanced exome	62
1058	normal	Day0	Enhanced exome	65
1058	tumor	Day0	Enhanced exome	72
1059	normal	C2D28	Enhanced exome	47
1059	tumor	C2D28	Enhanced exome	70
1059	tumor	Day0	Enhanced exome	69
1062	normal	Day0	RMG	336
1062	tumor	Day0	RMG	408
1063	tumor	C2D28	Enhanced exome	76
1063	normal	Day0	Enhanced exome	64
1063	tumor	Day0	Enhanced exome	78
1064	tumor	C2D28	Enhanced exome	76
1064	normal	Day0	Enhanced exome	65
1064	tumor	Day0	Enhanced exome	81
1002	tumor	Day0	AmpliSeq	2486
1004	tumor	Day0	AmpliSeq	1144
1010	tumor	Day0	AmpliSeq	2017
1011	tumor	Day0	AmpliSeq	1589
1013	tumor	Day0	AmpliSeq	1415
1014	tumor	Day0	AmpliSeq	1763
1017	tumor	Day0	AmpliSeq	1528
1019	tumor	Day0	AmpliSeq	2088
1023	tumor	Day0	AmpliSeq	1277
1035	tumor	Day0	AmpliSeq	2062
1036	tumor	Day0	AmpliSeq	2221
1037	tumor	Day0	AmpliSeq	2589
1041	tumor	Day0	AmpliSeq	2427
1047	tumor	Day0	AmpliSeq	2227

1048	tumor	Day0	AmpliSeq	1908
1049	tumor	Day0	AmpliSeq	2606
1052	tumor	Day0	AmpliSeq	4503
1058	tumor	Day0	AmpliSeq	2051
1061	tumor	Day0	AmpliSeq	3281
1062	tumor	Day0	AmpliSeq	2236
1063	tumor	Day0	AmpliSeq	1976
1065	tumor	Day0	AmpliSeq	3894
1066	tumor	Day0	AmpliSeq	4998
1067	tumor	Day0	AmpliSeq	5803
1068	tumor	Day0	AmpliSeq	4280
1069	tumor	Day0	AmpliSeq	5220
1070	tumor	Day0	AmpliSeq	3860
1072	tumor	Day0	AmpliSeq	4561
1073	tumor	Day0	AmpliSeq	4277
1074	tumor	Day0	AmpliSeq	3255
1076	tumor	Day0	AmpliSeq	3420
1077	tumor	Day0	AmpliSeq	3745
1078	tumor	Day0	AmpliSeq	4731
1079	tumor	Day0	AmpliSeq	4957
1080	tumor	Day0	AmpliSeq	3606
1084	tumor	Day0	AmpliSeq	4084
1085	tumor	Day0	AmpliSeq	4769
1088	tumor	Day0	AmpliSeq	3867
1089	tumor	Day0	AmpliSeq	4139
1090	tumor	Day0	AmpliSeq	6626
790809	tumor	Day0	AmpliSeq	3313
800684	tumor	Day0	AmpliSeq	2253
UC1	tumor	Day0	AmpliSeq	3833
UC10	tumor	Day0	AmpliSeq	3536
UC11	tumor	Day0	AmpliSeq	3102
UC12	tumor	Day0	AmpliSeq	2732
UC13	tumor	Day0	AmpliSeq	2959
UC14	tumor	Day0	AmpliSeq	3559
UC15	tumor	Day0	AmpliSeq	4328
UC16	tumor	Day0	AmpliSeq	605
UC17	tumor	Day0	AmpliSeq	3336
UC18	tumor	Day0	AmpliSeq	3553
UC2	tumor	Day0	AmpliSeq	3287
UC20	tumor	Day0	AmpliSeq	2426
UC21	tumor	Day0	AmpliSeq	3046

UC22	tumor	Day0	AmpliSeq	3106
UC23	tumor	Day0	AmpliSeq	3490
UC24	tumor	Day0	AmpliSeq	2974
UC26	tumor	Day0	AmpliSeq	2699
UC3	tumor	Day0	AmpliSeq	3066
UC4	tumor	Day0	AmpliSeq	3286
UC5	tumor	Day0	AmpliSeq	34
UC6	tumor	Day0	AmpliSeq	3269
UC7	tumor	Day0	AmpliSeq	4051
UC8	tumor	Day0	AmpliSeq	3390
UC9	tumor	Day0	AmpliSeq	3114

Table S2. Adverse events during cycles 1 and 2

	Events (percent of patients affected)
Infectious event	93 (66)
bacteremia	9 (9.4)
cellulitis	6 (7)
neutropenic fever	54 (41)
sepsis	5 (6)
lung infection	14 (11)
Arthralgia	2 (2)
Delirium	2 (2)
Diarrhea	2 (2)
Constipation	2 (2)
Fatigue	2 (2)
Stroke	1 (1)
DVT	3 (4)
Fall	2 (2)
Edema	1 (1)
Bleeding	5 (6)
Transfusion reaction	4 (3)
Sweet syndrome	2 (1)
Rash	1 (1)
Acute kidney injury	2 (2)
Cardiac arrest	1 (1)
STEMI	2 (2)
Atrial fibrillation	1 (1)

Table S3. Mutations identified through enhanced exome and 264 gene (RMG) panel analysis

Patient	Gene	Amino Acid Change		Chromosome	Start	Stop	Reference	Variant	Mutation Type		EnsemblGeneID	Normal Reference Count	Normal Variant Count	Normal Variant		Tumor		Tumor Variant	
		Change	Chromosome						Type	Tier				Allele Frequency	Count	Reference Count	Variant Count	Allele Frequency	Count
322879	TERT	NULL	5	1295228	1295228	G	A	SNP	tier4	ENSG00000164362	279	2	0.71	248	23	8.49			
322879	NF1	p.L2330V	17	29667589	29667589	T	G	SNP	tier1	ENSG00000196712	323	4	1.22	343	30	8.04			
371766	TET2	p.R1179fs	4	106164024	106164030	AAGAGTC	-	DEL	tier1	ENSG00000168769	149	2	1.32	123	25	16.89			
371766	NPM1	p.W288fs	5	170837546	170837547	-	GTAA	INS	tier1	ENSG00000181163	228	4	1.72	194	61	23.92			
371766	SRSF2	p.P95R	17	74732959	74732959	G	C	SNP	tier1	ENSG00000161547	451	13	2.8	276	185	40.04			
505186	IDH2	p.R140Q	15	90631934	90631934	C	T	SNP	tier1	ENSG00000182054	272	28	9.3	158	131	45.17			
		p.PPDSSHRSR95i				GTGTGAGTCGG													
505186	SRSF2	n_frame_del	17	74732936	74732959	GGG	-	DEL	tier1	ENSG00000161547	409	7	1.68	287	35	10.87			
654840	COL12A1	e10+10	6	75890645	75890645	C	T	SNP	tier3	ENSG00000111799	148	3	1.99	90	65	41.94			
654840	WT1	p.T273fs	11	32449554	32449555	-	G	INS	tier1	ENSG00000184937	218	2	0.91	123	91	42.52			
654840	CEBPA	p.N321K	19	33792358	33792358	A	T	SNP	tier1	ENSG00000245848	478	17	3.42	259	209	44.66			
						CGTACCTCTTCC													
654840	RUNX1	e4+5	21	36252848	36252849	-	ACTTCGAC	INS	tier3	ENSG00000159216	374	0	0	269	20	6.92			
692847	DDX41	p.R525H	5	176939370	176939370	C	T	SNP	tier1	ENSG00000183258	322	0	0	283	77	21.33			
692847	DDX41	p.D344G	5	176940753	176940753	T	C	SNP	tier1	ENSG00000183258	256	1	0.39	270	48	15			
692847	JAK2	p.V617F	9	5073770	5073770	G	T	SNP	tier1	ENSG00000096968	239	0	0	236	40	14.49			
790809	DNMT3A	p.A145T	2	25505325	25505325	C	T	SNP	tier1	ENSG00000119772	306	0	0	302	18	5.61			
790809	TP53	e4-1	17	7578555	7578555	C	T	SNP	tier1	ENSG00000141510	408	0	0	341	38	10			
790809	U2AF1	p.S34F	21	44524456	44524456	G	A	SNP	tier1	ENSG00000160201	338	0	0	289	28	8.83			
800684	CBL	p.Y371H	11	119148891	119148891	T	C	SNP	tier1	ENSG00000110395	242	1	0.41	123	8	6.11			
800684	CBL	p.C384Y	11	119148931	119148931	G	A	SNP	tier1	ENSG00000110395	300	1	0.33	134	36	21.18			
800684	TP53	p.A161T	17	7578449	7578449	C	T	SNP	tier1	ENSG00000141510	562	7	1.23	370	252	40.45			
800684	TP53	e4-2	17	7578556	7578556	T	C	SNP	tier1	ENSG00000141510	334	0	0	190	153	44.35			
548417	NPM1	amino_acid_change	5	170837543	170837544	-	TCTG	INS	tier1	ENSG00000181163	94	6	6	69	31	31			
						TCATATTCTCTG													
		amino_acid_change				AAATCAACGTA													
548417	FLT3	amino_acid_change	13	28608262	28608263	-	CCGGTCACG	INS	tier1	ENSG00000122025	99	1	1	97	3	3			
1013	GRID1	p.D170	10	87966131	87966131	G	A	SNP	tier1	ENSG00000182771	374	7	1.84	172	121	41.3			
1013	MUC5B	p.A668	11	1253930	1253930	G	A	SNP	tier1	ENSG00000117983	416	0	0	364	14	3.7			
1013	TP53	p.V216M	17	7578203	7578203	C	T	SNP	tier1	ENSG00000141510	422	8	1.86	75	291	79.29			
1037	SBF1P1	NULL	8	56365970	56365970	G	A	SNP	tier3	ENSG00000248522	428	0	0	561	22	3.77			
1037	TP53	p.R273H	17	7577120	7577120	C	T	SNP	tier1	ENSG00000141510	200	0	0	414	45	9.78			
1037	TP53	p.H179P	17	7578394	7578394	T	G	SNP	tier1	ENSG00000141510	343	0	0	592	73	10.94			
1037	KIF2B	p.A112T	17	51900728	51900728	G	A	SNP	tier1	ENSG00000141200	351	2	0.57	489	62	11.21			
1038	NRAS	p.G12D	1	115258747	115258747	C	T	SNP	tier1	ENSG00000213281	199	0	0	248	27	9.82			
1038	TET2	p.R1216*	4	106164778	106164778	C	T	SNP	tier1	ENSG00000168769	202	16	7.34	204	133	39.47			
1038	CBL	p.I383T	11	119148928	119148928	T	C	SNP	tier1	ENSG00000110395	182	19	9.41	110	254	69.78			
1038	MIR142	NULL	17	56408611	56408612	-	CCCCCTCGGGG	INS	tier1	ENSG00000207567	169	0	0	217	8	3.56			
1038	MIR142	NULL	17	56408626	56408626	A	G	SNP	tier1	ENSG00000207567	186	3	1.59	206	32	13.45			
1038	SRSF2	p.P95H	17	74732959	74732959	G	T	SNP	tier1	ENSG00000161547	227	17	6.97	292	221	43.08			
1038	MYO5B	p.R895Q	18	47429091	47429091	C	T	SNP	tier1	ENSG00000167306	276	1	0.36	302	30	9.04			
1038	ASXL1	p.R693*	20	31022592	31022592	C	T	SNP	tier1	ENSG00000171456	324	2	0.61	378	227	37.46			
1038	RUNX1	p.R162K	21	36252877	36252877	C	T	SNP	tier1	ENSG00000159216	394	21	5.06	99	445	81.8			
1047	SPEG	e2+19	2	220326798	220326798	G	A	SNP	tier3	ENSG00000072195	187	0	0	218	13	5.63			
1047	TP53	p.H193R	17	7578271	7578271	T	C	SNP	tier1	ENSG00000141510	287	2	0.69	381	73	16.01			
1048	MLL3	NULL	7	152132878	152132878	C	T	SNP	tier2	ENSG00000055609	286	1	0.35	165	131	44.11			

1048	TP53	p.R282W	17	7577094	7577094 G	A	SNP	tier1	ENSG00000141510	321	6	1.83	71	182	71.65
1048	PTPRT	p.R857H	20	40790170	40790170 C	T	SNP	tier1	ENSG00000196090	246	0	0	155	118	43.07
1057	RUNX1T1	p.A508V	8	92982935	92982935 G	A	SNP	tier1	ENSG00000079102	375	9	2.34	209	181	45.94
1057	PTPN11	p.A72V	12	112888199	112888199 C	T	SNP	tier1	ENSG00000179295	206	1	0.48	294	55	15.76
1057	SETBP1	p.D868N	18	42531907	42531907 G	A	SNP	tier1	ENSG00000152217	388	1	0.26	254	89	25.95
CACCACTGCCA															
1057	ASXL1	p.H633fs	20	31022403	31022425 TAGAGAGCG	-	DEL	tier1	ENSG00000171456	559	4	0.71	432	53	10.93
1062	TP53	p.L257P	17	7577511	7577511 A	G	SNP	tier1	ENSG00000141510	164	2	1.2	119	55	31.61
1062	TP53	p.H193L	17	7578271	7578271 T	A	SNP	tier1	ENSG00000141510	340	3	0.87	160	158	49.69
1001	PRAMEF7	p.V298I	1	12979700	12979700 G	A	SNP	tier1	ENSG00000204510	136	0	0	118	10	7.81
1001	CD1D	p.A257D	1	158152830	158152830 C	A	SNP	tier1	ENSG00000158473	81	0	0	40	40	49.38
1001	SWT1	p.P224R	1	185143950	185143950 C	G	SNP	tier1	ENSG00000116668	61	1	1.61	43	41	48.81
1001	NRG3	p.T166I	10	83635593	83635593 C	T	SNP	tier1	ENSG00000185737	77	3	3.75	45	30	40
1001	DMBT1	p.I3fs	10	124320291	124320292 -	A	INS	tier1	ENSG00000187908	58	0	0	25	16	39.02
1001	MTA2	p.Y283C	11	62364143	62364143 T	C	SNP	tier1	ENSG00000149480	239	4	1.65	184	140	43.21
1001	MMP13	p.F74	11	102826121	102826121 G	A	SNP	tier1	ENSG00000137745	62	1	1.56	25	27	51.92
1001	ENSG00000258423	NULL	14	52223853	52223853 C	T	SNP	tier3	ENSG00000258423	85	0	0	39	34	46.58
1001	ADAMTS17	p.R528H	15	100672350	100672350 C	T	SNP	tier1	ENSG00000140470	93	1	1.06	31	23	42.59
1001	HS3ST4	p.G366R	16	26147294	26147294 G	A	SNP	tier1	ENSG00000182601	56	0	0	44	5	10.2
1001	ENSG00000261436	NULL	16	60393322	60393322 G	C	SNP	tier3	ENSG00000261436	114	2	1.72	46	30	39.47
1001	SRSF2	p.P95H	17	74732959	74732959 G	T	SNP	tier1	ENSG00000161547	111	3	2.63	95	65	40.37
1001	LENG8	p.S122F	19	54964774	54964774 C	T	SNP	tier1	ENSG00000167615	61	1	1.61	58	33	36.26
1001	CACNA2D3	p.F239	3	54603862	54603862 C	T	SNP	tier1	ENSG00000157445	326	10	2.98	152	139	47.6
1001	SORCS2	p.Y1018	4	7731385	7731385 C	T	SNP	tier1	ENSG00000184985	70	0	0	32	25	43.86
1001	TET2	p.A1153V	4	106162544	106162544 C	T	SNP	tier1	ENSG00000168769	317	5	1.55	145	126	46.49
1001	TET2	p.Q1524*	4	106196237	106196237 C	T	SNP	tier1	ENSG00000168769	467	10	2.09	231	232	49.79
1001	PRDM9	p.G614	5	23527039	23527039 G	A	SNP	tier1	ENSG00000164256	75	1	1.32	54	29	34.94
1001	NR2E1	e2+13	6	108492820	108492820 G	A	SNP	tier3	ENSG00000112333	81	2	2.41	40	46	53.49
1001	ENSG00000213261	NULL	7	131347007	131347007 A	G	SNP	tier3	ENSG00000213261	61	0	0	44	31	41.33
1001	CSMD1	e68-91	8	2807956	2807956 G	C	SNP	tier3	ENSG00000183117	146	6	3.95	73	65	47.1
1001	FAM75A7	p.P393	9	65506381	65506381 G	A	SNP	tier1	ENSG00000234734	75	3	3.85	76	31	28.97
1001	STAG2	p.L203fs	X	123179149	123179150 -	TCATT	INS	tier1	ENSG00000101972	78	0	0	30	66	68.75
1002	U2AF1	p.S34F	21	44524456	44524456 G	A	SNP	tier1	ENSG00000160201	183	3	1.6	115	72	38.5
1002	JAK2	p.V617F	9	5073770	5073770 G	T	SNP	tier1	ENSG00000096968	201	1	0.5	121	69	36.32
1002	MYSM1	p.V505	1	59139302	59139302 G	A	SNP	tier1	ENSG00000162601	74	0	0	57	12	17.39
1002	ZNF687	p.Q389*	1	151259932	151259932 C	T	SNP	tier1	ENSG00000143373	242	3	1.22	231	7	2.94
1002	CACNA1E	p.T2129M	1	181765981	181765981 C	T	SNP	tier1	ENSG00000198216	126	10	7.35	62	46	42.59
1002	BRSK2	e19-16	11	1480406	1480406 C	T	SNP	tier2	ENSG00000174672	77	3	3.75	25	24	48.98
1002	KRTAP5-1	p.P145S	11	1606047	1606047 G	A	SNP	tier1	ENSG00000205869	98	0	0	70	13	15.66
1002	OR4A5	p.L99I	11	51412101	51412101 G	T	SNP	tier1	ENSG00000221840	48	3	5.88	32	30	48.39
1002	CTAGE10P	NULL	13	50466856	50466856 G	C	SNP	tier2	ENSG00000181358	189	0	0	145	16	9.94
1002	OLFM4	p.K220	13	53617329	53617329 G	A	SNP	tier1	ENSG00000102837	49	3	5.77	32	38	54.29
1002	TP53	p.G245S	17	7577548	7577548 C	T	SNP	tier1	ENSG00000141510	159	3	1.85	87	57	39.58
1002	NPTX1	p.H345Q	17	78445574	78445574 G	T	SNP	tier1	ENSG00000171246	66	3	4.35	27	28	50.91
1002	DNMT3A	e22-1	2	25457290	25457290 C	T	SNP	tier1	ENSG00000119772	75	5	6.17	29	32	52.46
1002	ENSG00000233991	NULL	2	91793509	91793509 G	A	SNP	tier4	ENSG00000233991	159	0	0	130	22	14.47
1002	ZNF355P	NULL	21	14485412	14485412 C	T	SNP	tier3	ENSG00000168122	113	0	0	95	15	13.64
1002	RUNX1	p.F396fs	21	36164687	36164688 -	TC	INS	tier1	ENSG00000159216	191	3	1.55	112	48	30
1002	DNAL4	p.N505	22	39176935	39176935 T	C	SNP	tier1	ENSG00000100246	56	1	1.75	47	21	30.88
1002	MLC1	NULL	22	50500004	50500004 T	G	SNP	tier3	ENSG00000100427	67	3	4.29	37	23	38.33
1002	MBNL1	p.N307D	3	152165466	152165466 A	G	SNP	tier1	ENSG00000152601	69	2	2.82	34	23	40.35
1002	LNX1	p.T59	4	54439993	54439993 G	A	SNP	tier1	ENSG00000072201	213	5	2.28	129	59	31.38
1002	TET2	e4+5	4	106164940	106164940 G	A	SNP	tier3	ENSG00000168769	137	10	6.8	49	43	46.74
1002	DDX60	e33-1	4	169146828	169146828 C	G	SNP	tier1	ENSG00000137628	77	2	2.53	43	32	42.67
1002	EPHA7	p.P897T	6	93956547	93956547 G	T	SNP	tier1	ENSG00000135333	66	2	2.94	53	14	20.9
1003	HIST2H2BE	p.N85S	1	149857937	149857937 T	C	SNP	tier1	ENSG00000184678	105	6	5.41	65	54	45.38

1003	FXYD4	NULL	10	43869150	43869150 G	A	SNP	tier3	ENSG00000150201	63	3	4.55	40	18	30
1003	DMBT1	p.L166V	10	124336127	124336127 C	G	SNP	tier1	ENSG00000187908	144	8	5.26	80	47	36.43
1003	LOC440041	NULL	11	55062331	55062331 G	T	SNP	tier3	ENSG00000166007	86	5	5.49	53	34	39.08
1003	PUS3	NULL	11	125818308	125818308 C	T	SNP	tier3	ENSG00000110060	61	0	0	24	22	47.83
1003	SNX29P2	e5-2796	16	29516967	29516967 A	T	SNP	tier3	ENSG00000198106	261	3	1.14	243	75	23.58
1003	NF1	e2-2	17	29482999	29482999 A	G	SNP	tier1	ENSG00000196712	238	11	4.33	150	103	39.46
1003	NF1	e3-2	17	29486026	29486026 A	G	SNP	tier1	ENSG00000196712	237	4	1.66	149	54	26.6
1003	SRSF2	p.P95L	17	74732959	74732959 G	A	SNP	tier1	ENSG00000161547	138	2	1.43	89	68	43.31
1003	TERF1P2	NULL	18	14392802	14392802 C	T	SNP	tier2	ENSG00000187589	105	5	4.55	49	33	40.24
1003	RUNX1	p.A351fs	21	36164821	36164822 -	GCCT	INS	tier1	ENSG00000159216	222	2	0.89	167	73	30.42
1003	TET2	p.C1289F	4	106180838	106180838 G	T	SNP	tier1	ENSG00000168769	268	21	7.27	34	220	86.61
1003	FCHO2	p.A4	5	72251935	72251935 G	A	SNP	tier1	ENSG00000157107	88	0	0	69	8	10.39
1003	FAM162B	p.A120S	6	117083172	117083172 C	A	SNP	tier1	ENSG00000183807	73	6	7.59	25	20	44.44
1003	MGAM	e4-23	7	141720751	141720751 A	G	SNP	tier3	ENSG00000257335	55	1	1.79	33	28	45.9
1003	MGAM	p.Q1326	7	141759685	141759685 G	A	SNP	tier1	ENSG00000257335	53	0	0	38	34	47.22
1003	ABCf2	e15-2171	7	150907364	150907364 C	T	SNP	tier3	ENSG00000033050	86	2	2.27	64	15	18.99
1003	DLC1	p.A220E	8	13356922	13356922 G	T	SNP	tier1	ENSG00000164741	477	8	1.65	334	227	40.46
1003	FGF17	p.H28Y	8	21903634	21903634 C	T	SNP	tier1	ENSG00000158815	57	0	0	43	18	29.51
1003	DENND3	p.V53M	8	142148132	142148132 G	A	SNP	tier1	ENSG00000105339	89	0	0	94	0	0
1003	SMC1A	p.R208P	X	53440081	53440081 C	G	SNP	tier1	ENSG0000072501	274	0	0	234	0	0
1003	SRPK3	e2+26	X	153046827	153046827 G	A	SNP	tier2	ENSG00000184343	65	2	2.99	27	28	50.91
1004	MRPL55	NULL	1	228295840	228295840 T	A	SNP	tier1	ENSG00000162910	118	0	0	104	55	34.59
1004	LIPM	p.S138F	10	90573001	90573001 C	T	SNP	tier1	ENSG00000173239	69	1	1.43	35	32	47.76
1004	ZNF664	NULL	12	124498724	124498724 G	C	SNP	tier4	ENSG00000179195	67	0	0	97	0	0
1004	TP53	p.Y126C	17	7578553	7578553 T	C	SNP	tier1	ENSG00000141510	90	1	1.1	48	95	66.43
1004	FCGBP	p.G616R	19	40424357	40424357 C	G	SNP	tier1	ENSG00000090920	166	0	0	297	0	0
1004	DNMT3A	p.L737P	2	25463283	25463283 A	G	SNP	tier1	ENSG00000119772	160	0	0	251	4	1.57
1004	ZNF831	p.D275H	20	57766897	57766897 G	C	SNP	tier1	ENSG00000124203	85	0	0	52	28	34.57
1004	ABI3BP	e7-32	3	100595436	100595436 G	A	SNP	tier3	ENSG00000154175	62	0	0	44	28	38.89
1004	BBX	p.P762L	3	107508175	107508175 C	T	SNP	tier1	ENSG00000114439	106	0	0	94	1	1.05
1004	ENSG00000181495	p.H22D	5	32789571	32789571 C	G	SNP	tier1	ENSG00000181495	53	0	0	51	0	0
1004	SH3TC2	NULL	5	148381839	148381839 C	T	SNP	tier3	ENSG00000169247	108	0	0	13	36	73.47
1004	FREM1	p.V1787A	9	14756422	14756422 A	G	SNP	tier1	ENSG00000164946	110	1	0.89	70	38	35.19
1004	SHROOM2	e1+3083	X	9757833	9757833 G	A	SNP	tier3	ENSG00000146950	78	0	0	81	69	45.39
1004	PCDH11X	p.S231I	X	91131931	91131931 G	T	SNP	tier1	ENSG00000102290	98	0	0	80	48	37.21
1004	ENSG00000203930	p.L12	X	139793812	139793812 G	A	SNP	tier1	ENSG00000203930	54	0	0	39	37	48.68
1005	CROCCP2	NULL	1	16953026	16953026 G	C	SNP	tier3	ENSG00000215908	460	0	0	417	0	0
1005	MACF1	p.R3138K	1	39854113	39854113 G	A	SNP	tier1	ENSG00000127603	63	0	0	45	9	16.67
1005	HRNR	p.H1936	1	152188297	152188297 G	A	SNP	tier1	ENSG00000197915	233	0	0	193	12	5.85
1005	WT1	p.H359Y	11	32421517	32421517 G	A	SNP	tier1	ENSG00000184937	148	0	0	200	7	3.38
1005	ENSG00000220948	NULL	11	48997309	48997309 T	C	SNP	tier3	ENSG00000220948	179	0	0	137	33	19.41
1005	KRTAP5-10	NULL	11	71276586	71276586 C	T	SNP	tier3	ENSG00000204572	98	0	0	85	15	15
1005	FAR2	p.V281	12	29464035	29464035 C	T	SNP	tier1	ENSG0000064763	68	0	0	77	16	17.2
1005	PLEKHA8P1	NULL	12	45567638	45567638 A	C	SNP	tier3	ENSG00000134297	60	1	1.64	32	14	29.79
1005	DDX54	p.A703G	12	113600824	113600824 G	C	SNP	tier1	ENSG00000123064	80	0	0	95	0	0
1005	UBE2L5P	NULL	13	31002620	31002620 G	C	SNP	tier2	ENSG00000236444	135	0	0	132	0	0
1005	IGHG1	p.M135I	14	106208495	106208495 C	G	SNP	tier1	ENSG00000211896	118	0	0	88	0	0
1005	ALDH1A2	NULL	15	58458849	58458849 G	C	SNP	tier3	ENSG00000128918	88	0	0	85	0	0
1005	VPS13C	p.A1583T	15	62241654	62241654 C	T	SNP	tier1	ENSG00000129003	76	0	0	67	24	26.37
1005	MYO1C	e19+79	17	1375122	1375122 C	G	SNP	tier2	ENSG00000197879	67	0	0	61	0	0
1005	KRTAP4-8	NULL	17	39253748	39253748 G	A	SNP	tier2	ENSG00000204880	60	0	0	51	12	19.05
1005	EMR1	p.E338	19	6906508	6906508 G	A	SNP	tier1	ENSG00000174837	70	0	0	67	11	14.1
1005	ROCK2	e30+25	2	11333880	11333880 C	A	SNP	tier2	ENSG00000134318	70	1	1.41	61	11	15.28
1005	TTN	p.A9658	2	179549073	179549073 C	T	SNP	tier1	ENSG00000155657	60	0	0	47	10	17.54
1005	MYO1B	e10-1	2	192228883	192228883 G	C	SNP	tier1	ENSG00000128641	58	0	0	64	0	0
1005	MLPH	p.V21A	2	238402131	238402131 T	C	SNP	tier1	ENSG00000115648	69	1	1.43	45	8	15.09

1005	KCNQ2	e17-9	20	62038737	62038737 G	C	SNP	tier2	ENSG0000075043	103	0	0	82	0	0
1005	HSCB	p.K231	22	29153142	29153142 G	A	SNP	tier1	ENSG00000100209	72	0	0	81	0	0
1005	INPP5J	p.G139A	22	31521141	31521141 G	C	SNP	tier1	ENSG00000185133	61	0	0	63	0	0
1005	EIF4ENIF1	p.P317A	22	31854475	31854475 G	C	SNP	tier1	ENSG00000184708	205	0	0	179	0	0
1005	CYP2D7P1	p.N45K	22	42540331	42540331 G	C	SNP	tier1	ENSG00000205702	93	1	1.06	100	0	0
1005	MAPK8IP2	p.G760A	22	51045398	51045398 G	C	SNP	tier1	ENSG0000008735	72	0	0	77	1	1.28
1005	MAPK8IP2	p.E818Q	22	51049187	51049187 G	C	SNP	tier1	ENSG0000008735	75	0	0	96	0	0
1005	LRRC2	p.L169	3	46574385	46574385 G	A	SNP	tier1	ENSG00000163827	70	0	0	67	0	0
1005	TBC1D23	e2+8	3	99998612	99998612 G	C	SNP	tier3	ENSG0000036054	110	0	0	121	0	0
1005	IMPG2	e19-30	3	100945855	100945855 -	A	INS	tier3	ENSG0000081148	49	2	3.92	34	14	29.17
1005	ZFYVE28	NULL	4	2343180	2343180 C	G	SNP	tier3	ENSG00000159733	74	0	0	70	0	0
1005	ENSG00000216819	NULL	6	3177396	3177396 C	G	SNP	tier3	ENSG00000216819	76	0	0	65	0	0
1005	MRPS18A	p.G12A	6	43655482	43655482 C	G	SNP	tier1	ENSG0000096080	110	0	0	122	0	0
1005	POLR2J	p.P4L	7	102119297	102119297 G	A	SNP	tier1	ENSG000005075	75	1	1.32	65	14	17.72
1005	ENSG00000236717	NULL	9	94951735	94951735 C	G	SNP	tier2	ENSG00000236717	65	0	0	69	0	0
1008	NRAS	p.Q61R	1	115256529	115256529 T	C	SNP	tier1	ENSG00000213281	283	4	1.39	165	140	45.9
1008	PIPSL	NULL	10	95720016	95720016 G	A	SNP	tier3	ENSG00000180764	68	0	0	33	34	50.75
1008	WDR11	p.I382K	10	122626231	122626231 T	A	SNP	tier1	ENSG00000120008	70	0	0	40	41	50.62
1008	ENSG00000254751	NULL	11	89510407	89510407 G	A	SNP	tier3	ENSG00000254751	79	1	1.25	62	35	36.08
1008	SNAPC1	p.D22G	14	62229243	62229243 A	G	SNP	tier1	ENSG0000023608	74	1	1.33	40	35	46.67
1008	ENSG00000259962	NULL	16	53397560	53397560 G	A	SNP	tier3	ENSG00000259962	119	2	1.64	75	88	53.99
1008	KIFC3	p.P807S	16	57793697	57793697 G	A	SNP	tier1	ENSG00000140859	56	0	0	30	31	50.82
1008	MYH1	p.R716K	17	10409156	10409156 C	T	SNP	tier1	ENSG00000109061	140	0	0	109	74	40.44
1008	TTR	e2+44	18	29173033	29173033 C	T	SNP	tier2	ENSG00000118271	57	0	0	20	21	51.22
1008	LOC100653346	NULL	19	182771	182771 A	G	SNP	tier3	ENSG00000206082	347	2	0.57	303	89	22.7
1008	CACNA1A	p.E722	19	13414369	13414369 C	T	SNP	tier1	ENSG00000141837	79	2	2.47	83	14	14.43
1008	ALLC	p.D278N	2	3745028	3745028 G	A	SNP	tier1	ENSG00000151360	57	1	1.72	50	42	45.65
1008	ENSG00000223703	NULL	2	91925152	91925152 G	A	SNP	tier2	ENSG00000223703	117	4	3.31	75	54	41.54
1008	FAP	NULL	2	163054192	163054192 G	A	SNP	tier3	ENSG00000078098	61	3	4.69	37	35	48.61
1008	CPS1	p.N758	2	211473148	211473148 C	T	SNP	tier1	ENSG0000021826	66	2	2.94	28	42	60
1008	ANKRD20A11P	NULL	21	15310389	15310389 C	T	SNP	tier1	ENSG00000215559	63	1	1.56	36	37	50.68
1008	ARPC4	NULL	3	9834714	9834714 C	A	SNP	tier2	ENSG00000241553	80	0	0	51	36	41.38
1008	BOD1L	e26-2744	4	13574496	13574496 T	A	SNP	tier3	ENSG0000038219	66	3	4.35	47	45	48.91
1008	TXK	e10+4	4	48088479	48088479 G	A	SNP	tier3	ENSG0000074966	58	4	6.45	33	39	54.17
1008	MEF2C	p.H174N	5	88047743	88047743 G	T	SNP	tier1	ENSG0000081189	84	1	1.16	71	58	44.96
1008	DDX41	p.R479	5	176939611	176939611 G	T	SNP	tier1	ENSG00000183258	224	2	0.88	127	142	52.4
1008	RASA4	e1-24	7	102279670	102279670 A	C	SNP	tier3	ENSG00000105808	102	6	5.56	37	13	26
1008	ENSG00000253228	NULL	8	1089696122	1089696122 C	A	SNP	tier3	ENSG00000253228	61	0	0	35	31	46.97
1008	HMCN2	e6-35	9	133057910	133057910 G	T	SNP	tier3	ENSG00000148357	53	3	5.36	27	28	49.12
1008	TMEM27	e1+35	X	15682806	15682806 C	G	SNP	tier3	ENSG00000147003	72	2	2.7	6	65	91.55

AAAGACTCCCA

TTTGAGATCAT

ATTCAATTCTC

1009	FLT3	ITD	13	28608283	28608284 -	TGAAATCAACG	INS	tier1	ENSG00000122025	291	0	0	197	0	0
1009	CELA3A	p.R190S	1	22333936	22333936 G	C	SNP	tier1	ENSG00000142789	61	0	0	33	0	0
1009	MAST2	p.R222H	1	46463468	46463468 G	A	SNP	tier1	ENSG00000086015	92	1	1.08	47	37	44.05
1009	DEGS1	NULL	1	224363570	224363570 G	T	SNP	tier3	ENSG00000143753	123	0	0	76	0	0
1009	NCAM1	NULL	11	112832085	112832085 G	C	SNP	tier2	ENSG00000149294	122	0	0	120	0	0
1009	A2M	p.T306	12	9259163	9259163 G	C	SNP	tier1	ENSG00000175899	71	0	0	39	0	0
1009	ENSG00000233732	NULL	16	33006576	33006576 G	T	SNP	tier2	ENSG00000233732	138	0	0	93	0	0
1009	CBFB	p.R43G	16	67063678	67063678 C	G	SNP	tier1	ENSG0000067955	103	1	0.96	51	22	30.14
1009	ZNF780A	e2+26	19	40588992	40588992 A	G	SNP	tier3	ENSG00000197782	77	0	0	30	27	47.37
1009	VSIG10L	p.L772	19	51837550	51837550 A	G	SNP	tier1	ENSG00000186806	90	1	1.1	32	27	45.76
1009	SLC9B1P2	NULL	2	92071232	92071232 C	G	SNP	tier2	ENSG00000214329	161	0	0	112	0	0
1009	ENSG00000204253	NULL	2	190788300	190788300 T	C	SNP	tier3	ENSG00000204253	64	0	0	52	0	0

1009	KIF1A	p.F955	2	241689958	241689958 G	A	SNP	tier1	ENSG00000130294	58	0	0	21	15	41.67
1009	ENSG00000251287	NULL	3	129814832	129814832 G	A	SNP	tier3	ENSG00000251287	164	2	1.2	77	51	39.84
1009	SI	p.R1230H	3	164735406	164735406 C	T	SNP	tier1	ENSG0000009402	255	3	1.16	102	84	45.16
1009	LIMCH1	p.P881L	4	41648732	41648732 C	T	SNP	tier1	ENSG00000064042	72	0	0	27	15	35.71
1009	KIT	p.W557R	4	55593603	55593603 T	C	SNP	tier1	ENSG00000157404	303	0	0	200	3	1.47
1009	YTHDC1	NULL	4	69179066	69179066 T	C	SNP	tier3	ENSG00000083896	64	0	0	23	15	39.47
1009	CTNND2	p.D823N	5	11098857	11098857 C	T	SNP	tier1	ENSG00000169862	59	2	3.28	30	18	37.5
1009	PCDHA7	p.A744T	5	140216198	140216198 G	A	SNP	tier1	ENSG00000204963	136	0	0	99	0	0
1009	LOC643201	NULL	5	175574083	175574083 G	A	SNP	tier3	ENSG00000248596	51	0	0	17	16	48.48
1009	PHIP	NULL	6	79787857	79787857 C	G	SNP	tier2	ENSG00000146247	76	0	0	49	0	0
1009	ENPP1	p.N812	6	132206195	132206195 T	C	SNP	tier1	ENSG00000197594	68	0	0	28	23	45.1
1009	COL1A2	e45-7	7	94055728	94055728 T	C	SNP	tier3	ENSG00000164692	67	0	0	45	3	6.25
1009	SLC26A3	e13+38	7	107417044	107417044 C	G	SNP	tier3	ENSG00000091138	61	0	0	35	0	0
1009	FAM90A25P	NULL	8	12272665	12272665 C	T	SNP	tier3	ENSG00000251402	57	0	0	33	17	34
1009	RPL7	e4+44	8	74203964	74203964 T	A	SNP	tier3	ENSG00000147604	69	0	0	21	17	44.74
1009	RPL7	e4+42	8	74203966	74203966 A	G	SNP	tier3	ENSG00000147604	68	0	0	21	17	44.74
1009	DENND3	p.K1106N	8	142202684	142202684 G	C	SNP	tier1	ENSG00000105339	73	0	0	55	0	0
1009	GLIS3	e6-1243	9	3900078	3900078 G	C	SNP	tier4	ENSG00000107249	105	4	3.67	35	37	51.39
1010	IDH2	p.R172K	15	90631838	90631838 C	T	SNP	tier1	ENSG00000182054	205	0	0	143	133	48.19
1010	SF3B1	p.K700E	2	198266834	198266834 T	C	SNP	tier1	ENSG00000115524	102	0	0	59	66	52.8
1010	KAT6B	p.D1237fs	10	76788292	76788293 AC	-	DEL	tier1	ENSG00000156650	61	0	0	61	34	35.79
1010	PRMT8	p.I183N	12	3677938	3677938 T	A	SNP	tier1	ENSG00000111218	58	0	0	31	40	56.34
1010	MIEPEP	p.A95V	13	24460551	24460551 G	A	SNP	tier1	ENSG0000027001	91	0	0	52	43	44.79
1010	RRN3P2	NULL	16	29110458	29110458 T	C	SNP	tier3	ENSG00000103472	62	1	1.56	89	9	8.91
1010	MYH13	p.Q477E	17	10248674	10248674 G	C	SNP	tier1	ENSG00000067888	156	0	0	96	107	52.45
1010	BAHCC1	p.R2313fs	17	79428627	79428627 G	-	DEL	tier1	ENSG00000171282	55	0	0	53	27	33.75
1010	CTAGE1	p.A435V	18	19996471	19996471 G	A	SNP	tier1	ENSG00000212710	67	0	0	50	40	43.96
1010	SPEG	p.E1509	2	220341671	220341671 G	A	SNP	tier1	ENSG00000072195	77	0	0	51	51	50
1010	PCDHA9	p.D483	5	140229529	140229529 C	T	SNP	tier1	ENSG00000204961	150	0	0	212	0	0
1010	DDC	p.A325V	7	50547532	50547532 G	A	SNP	tier1	ENSG00000132437	59	0	0	28	20	41.67
1010	PEX1	p.D545	7	92138678	92138678 G	A	SNP	tier1	ENSG00000127980	56	0	0	31	20	39.22
1010	NHS	p.N192H	X	17705870	17705870 A	C	SNP	tier1	ENSG00000188158	86	0	0	6	132	95.65
1011	DNMT3A	p.R882C	2	25457243	25457243 G	A	SNP	tier1	ENSG00000119772	155	0	0	175	14	7.41
1011	CACNA1A	p.R1672Q	19	13346498	13346498 C	T	SNP	tier1	ENSG00000141837	152	0	0	131	5	3.65
1011	SMOC2	p.T448M	6	169064778	169064778 C	T	SNP	tier1	ENSG00000112562	106	0	0	118	4	3.25
1012	RUNX1	p.R162S	21	36252876	36252876 C	A	SNP	tier1	ENSG00000159216	324	9	2.7	149	109	42.25
1012	GBP1	p.M11V	1	89528887	89528887 T	C	SNP	tier1	ENSG00000117228	104	6	5.45	48	25	34.25
1012	POLR3C	NULL	1	145610672	145610672 C	T	SNP	tier2	ENSG00000186141	48	2	3.92	24	30	55.56
1012	TRIM49L2	p.P47T	11	89768518	89768518 C	A	SNP	tier1	ENSG00000204449	116	0	0	48	50	51.02
1012	GALNT1	e4+44	14	69792165	69792165 G	A	SNP	tier3	ENSG00000100626	51	3	5.45	27	19	41.3
1012	SERPIN A6	p.F388	14	94770809	94770809 G	A	SNP	tier1	ENSG00000170099	99	1	1	33	35	51.47
1012	ADAMTS17	p.R222W	15	100821559	100821559 G	A	SNP	tier1	ENSG00000140470	96	4	3.88	38	20	33.33
1012	MUC16	p.L696	19	9089729	9089729 G	A	SNP	tier1	ENSG00000181143	295	7	2.32	138	129	48.13
1012	DOCK6	p.N1844S	19	11312722	11312722 T	C	SNP	tier1	ENSG00000130158	77	2	2.53	25	25	50
1012	ZFP36L2	NULL	2	43450743	43450744 -	A	INS	tier2	ENSG00000152518	52	0	0	28	19	40.43
1012	TRIM60	p.G357E	4	165962294	165962294 G	A	SNP	tier1	ENSG00000176979	57	4	6.56	43	12	21.82
1012	DNAH5	p.K388I	5	13735358	13735358 C	T	SNP	tier1	ENSG00000039139	262	5	1.87	159	122	43.42
1012	ZFR	p.T470	5	32403317	32403317 C	T	SNP	tier1	ENSG00000056097	60	2	3.23	41	27	39.71
1012	KCNU1	p.K1061*	8	36793169	36793169 A	T	SNP	tier1	ENSG00000215262	241	0	0	253	19	6.99
1014	ELTD1	p.W384S	1	79387404	79387404 C	G	SNP	tier1	ENSG00000162618	57	0	0	58	0	0
1014	ENSG00000239012	NULL	1	142653748	142653748 C	T	SNP	tier1	ENSG00000239012	325	0	0	275	2	0.72
1014	PRKCQ	p.R674W	10	6470270	6470270 G	A	SNP	tier1	ENSG00000065675	54	0	0	58	0	0
1014	GRID1	p.P952	10	87362204	87362204 C	T	SNP	tier1	ENSG00000182771	169	3	1.74	154	5	3.14
1014	C12orf77	p.P125S	12	25148775	25148775 G	A	SNP	tier1	ENSG00000226397	79	0	0	30	35	53.85
1014	LYRM5	p.K37R	12	25357083	25357083 A	G	SNP	tier1	ENSG00000205707	108	4	3.57	98	1	1.01
1014	TMPRSS12	p.N219	12	51279033	51279033 C	T	SNP	tier1	ENSG00000186452	83	3	3.49	55	38	40.86

1014	CCDC53	NULL	12	102437854	102437854 C	T	SNP	tier3	ENSG00000120860	54	0	0	33	22	40
1014	GLIS2	p.E268K	16	4386752	4386752 G	A	SNP	tier1	ENSG00000126603	65	0	0	17	36	67.92
1014	UBE2MP1	NULL	16	34404296	34404296 G	A	SNP	tier2	ENSG00000261461	112	0	0	20	28	58.33
1014	TPS3	p.L344P	17	7573996	7573996 A	G	SNP	tier1	ENSG00000141510	150	0	0	18	48	72.73
1014	GOSR1	e9-83	17	28849188	28849189 CA	-	DEL	tier2	ENSG00000108587	59	1	1.67	51	0	0
1014	PPM1D	p.R572*	17	58740809	58740809 C	T	SNP	tier1	ENSG00000170836	56	0	0	62	0	0
1014	RBFOX3	NULL	17	77086921	77086921 T	A	SNP	tier4	ENSG00000167281	73	0	0	47	32	40.51
1014	NOL4	p.V85	18	31802963	31802963 G	T	SNP	tier1	ENSG00000101746	59	0	0	32	0	0
1014	REEP6	p.T400	19	1497653	1497653 G	A	SNP	tier1	ENSG00000115255	103	1	0.96	63	45	41.67
1014	FKBP8	p.P83L	19	18652620	18652620 G	A	SNP	tier1	ENSG00000105701	224	2	0.88	249	1	0.4
1014	CRIM1	NULL	2	36776167	36776167 T	C	SNP	tier2	ENSG00000150938	163	2	1.21	105	56	34.78
1014	FEZ2	p.N313fs	2	36785621	36785622 -	T	INS	tier1	ENSG00000171055	51	0	0	39	0	0
1014	ZAK	e12-43	2	174096877	174096877 C	T	SNP	tier3	ENSG00000091436	65	0	0	39	19	32.76
		p.L10in_frame_-													
1014	ALPP	del	2	233243529	233243531 TGC	-	DEL	tier1	ENSG00000163283	97	0	0	84	1	1.18
1014	CCDC110	p.P785L	4	186379387	186379387 G	A	SNP	tier1	ENSG00000168491	65	0	0	79	0	0
1014	ENSG00000230648	NULL	6	4020389	4020389 A	T	SNP	tier2	ENSG00000230648	92	2	2.13	116	3	2.52
1014	C7orf57	e7-3	7	48094189	48094189 C	T	SNP	tier3	ENSG00000164746	53	1	1.85	20	22	52.38
1014	CHD7	p.K1865R	8	61763650	61763650 A	G	SNP	tier1	ENSG00000171316	65	0	0	38	13	25.49
1014	NHS	p.V190I	X	17705864	17705864 G	A	SNP	tier1	ENSG00000188158	172	1	0.58	26	133	83.65
1014	FAM47A	p.R412C	X	34149162	34149162 G	A	SNP	tier1	ENSG00000185448	192	1	0.52	227	0	0
1016	DNMT3A	p.R882C	2	25457243	25457243 G	A	SNP	tier1	ENSG00000119772	150	2	1.31	135	46	25.41
1016	ENSG00000231009	NULL	10	43191261	43191261 G	A	SNP	tier3	ENSG00000231009	62	0	0	60	11	15.49
1016	LRRC9	p.R858W	14	60468726	60468726 C	T	SNP	tier1	ENSG00000131951	59	2	3.28	45	12	21.05
1016	ONECUT2	NULL	18	55145779	55145779 T	C	SNP	tier2	ENSG00000119547	50	0	0	42	14	25
1016	TYK2	p.P216L	19	10476557	10476557 G	A	SNP	tier1	ENSG00000105397	71	1	1.39	125	20	13.79
1016	PSG5	NULL	19	43679231	43679231 T	G	SNP	tier3	ENSG00000204941	122	1	0.81	105	8	7.08
1016	LCLAT1	e3+9	2	30756189	30756189 T	C	SNP	tier2	ENSG00000172954	79	0	0	70	9	11.39
1016	DSCAM	e9-26	21	41684312	41684312 C	T	SNP	tier3	ENSG00000171587	330	0	0	287	11	3.69
1016	CD96	p.V512F	3	111366398	111366398 G	T	SNP	tier1	ENSG00000153283	80	0	0	62	12	16.22
1016	GATA2	p.N317S	3	128202770	128202770 T	C	SNP	tier1	ENSG00000179348	216	4	1.81	180	40	18.18
1016	C2	p.R16Q	6	31901496	31901496 G	A	SNP	tier1	ENSG00000166278	50	1	1.96	54	12	18.18
1016	ECT2L	p.R197H	6	139164363	139164363 G	A	SNP	tier1	ENSG00000203734	58	0	0	57	18	24
1016	FAM47A	p.D275	X	34149571	34149571 G	A	SNP	tier1	ENSG00000185448	540	6	1.1	364	127	25.87
1017	PAPPA2	p.R271W	1	176526269	176526269 C	T	SNP	tier1	ENSG00000116183	78	2	2.47	41	32	43.84
1017	GTPBP4	e6-14	10	1044929	1044929 C	A	SNP	tier3	ENSG00000107937	56	1	1.75	47	18	27.69
1017	NAV3	p.E1632D	12	78562561	78562561 A	T	SNP	tier1	ENSG00000067798	73	0	0	30	17	36.17
1017	KLHL1	p.H437N	13	70413213	70413213 G	T	SNP	tier1	ENSG00000150361	76	0	0	47	19	28.79
1017	KCNH5	p.N787	14	63174832	63174832 G	A	SNP	tier1	ENSG00000140015	66	2	2.94	40	25	38.46
1017	MTA1	p.S639fs	14	105936238	105936239 -	G	INS	tier1	ENSG00000182979	51	0	0	70	7	9.09
1017	TP53	p.Y234N	17	7577581	7577581 A	T	SNP	tier1	ENSG00000141510	161	6	3.59	70	118	62.77
1017	WIZ	e2-88	19	15551543	15551543 A	G	SNP	tier3	ENSG0000011451	55	0	0	40	22	35.48
1017	ATP5SL	NULL	19	42027504	42027504 A	G	SNP	tier2	ENSG00000105341	142	0	0	116	0	0
1017	LGALSL	p.L96Q	2	64685508	64685508 T	A	SNP	tier1	ENSG00000119862	49	2	3.92	42	19	31.15
1017	CLEC4F	p.L49F	2	71046938	71046938 C	A	SNP	tier1	ENSG00000152672	67	2	2.9	49	17	25.76
1017	TOP2B	e9-6	3	25674291	25674292 -	A	INS	tier3	ENSG00000077097	116	0	0	122	12	8.96
1017	KALRN	e13+5832	3	124123550	124123554 AATT	-	DEL	tier4	ENSG00000160145	95	0	0	79	21	21
1017	NKD2	e5-111	5	1033376	1033376 G	A	SNP	tier2	ENSG00000145506	55	2	3.45	37	20	35.09
1017	HMGXB3	p.A20	5	149384475	149384475 C	G	SNP	tier1	ENSG00000113716	59	3	4.84	25	11	30.56
1017	ECI2	p.A67	6	4133795	4133795 C	T	SNP	tier1	ENSG00000198721	63	2	3.08	43	23	34.85
1017	COL21A1	p.R613*	6	55942347	55942347 G	A	SNP	tier1	ENSG00000124749	185	3	1.6	119	61	33.89
1017	ABRACL	p.R16S	6	139355343	139355343 C	A	SNP	tier1	ENSG00000146386	60	0	0	75	0	0
1017	CNTNAP3	NULL	9	39085672	39085672 G	A	SNP	tier3	ENSG00000106714	185	0	0	217	0	0
1017	FAM75D1	p.S897T	9	84608074	84608074 T	A	SNP	tier1	ENSG00000214929	81	0	0	39	27	40.91
1017	PTCH1	p.Q1285	9	98209683	98209683 C	T	SNP	tier1	ENSG00000185920	139	11	7.33	114	52	31.14
1017	FAM47C	p.Q148	X	37026927	37026927 G	A	SNP	tier1	ENSG00000198173	150	8	5.06	35	92	72.44

1018	NRAS	p.Q61H	1	115256528	115256528 T	G	SNP	tier1	ENSG00000213281	264	0	0	345	40	10.39
1018	DNMT3A	p.R882C	2	25457243	25457243 G	A	SNP	tier1	ENSG00000119772	121	9	6.92	67	94	58.39
1018	IDH1	p.R132C	2	209113113	209113113 G	A	SNP	tier1	ENSG00000138413	202	6	2.87	170	109	39.07
1018	LOC645359	e1+57	1	13218943	13218943 G	T	SNP	tier3	ENSG00000229571	82	0	0	107	12	10.08
1018	OR2L13	e1-76744	1	248185208	248185209 -	C	INS	tier3	ENSG00000196071	55	0	0	38	28	42.42
1018	C11orf9	p.P289A	11	61539096	61539096 C	G	SNP	tier1	ENSG00000124920	78	2	2.5	41	33	44.59
1018	KSR2	e4+34	12	118198782	118198782 C	T	SNP	tier2	ENSG00000171435	171	6	3.39	124	97	43.89
1018	TRPM1	p.R1461H	15	31294572	31294572 C	T	SNP	tier1	ENSG00000134160	62	1	1.56	39	24	38.1
1018	ENSG00000259404	NULL	15	84752935	84752935 T	C	SNP	tier3	ENSG00000259404	67	2	2.9	33	35	51.47
1018	ZCCHC14	NULL	16	87439918	87439918 C	A	SNP	tier2	ENSG00000140948	99	4	3.88	94	55	36.91
1018	DNAH9	p.R318C	17	11520775	11520775 C	T	SNP	tier1	ENSG0000007174	183	4	2.13	149	112	42.91
1018	NOS2	NULL	17	26078168	26078168 G	A	SNP	tier2	ENSG0000007171	95	1	1.04	46	45	49.45
1018	SRSF2	p.P95L	17	74732959	74732959 G	A	SNP	tier1	ENSG00000161547	75	1	1.32	74	75	50
1018	CARD14	p.S983N	17	78182077	78182077 G	A	SNP	tier1	ENSG00000141527	52	2	3.7	60	49	44.95
1018	CACNA1A	e14-73	19	13419138	13419138 C	T	SNP	tier3	ENSG00000141837	61	1	1.61	61	53	46.49
1018	DNMT3A	p.R771*	2	25463182	25463182 G	A	SNP	tier1	ENSG00000119772	177	3	1.67	157	119	43.12
1018	TRIM43B	NULL	2	96146241	96146241 T	C	SNP	tier2	ENSG00000144010	73	0	0	73	4	5.19
1018	COL5A2	NULL	2	189898101	189898101 T	C	SNP	tier3	ENSG00000204262	138	0	0	91	79	46.47
1018	CECR2	p.R585Q	22	18020425	18020425 G	A	SNP	tier1	ENSG00000099954	219	0	0	235	182	43.65
1018	INPP4B	e8-5	4	143181722	143181723 -	A	INS	tier4	ENSG00000109452	103	0	0	110	8	6.78
1018	MDH2	NULL	7	75677463	75677463 C	A	SNP	tier2	ENSG00000146701	49	2	3.92	46	44	48.89
1018	SMC1A	p.R807H	X	53430498	53430498 C	T	SNP	tier1	ENSG00000072501	84	2	2.33	10	117	92.13
1019	SCAMP5	NULL	15	75311459	75311460 TA	-	DEL	tier4	ENSG00000198794	63	0	0	50	6	10.71
1019	TP53	p.R175G	17	7578407	7578407 G	C	SNP	tier1	ENSG00000141510	356	3	0.83	54	441	89.09
1019	MYO5B	p.R829H	18	47431127	47431127 C	T	SNP	tier1	ENSG00000167306	367	2	0.54	40	187	82.02
1019	MYO1B	p.V843	2	192267417	192267417 C	T	SNP	tier1	ENSG00000128641	59	0	0	41	13	24.07
1019	ZHX3	p.P912	20	39813740	39813740 C	T	SNP	tier1	ENSG00000174306	95	0	0	58	34	36.96
1019	QTRTD1	p.L347P	3	113804543	113804543 T	C	SNP	tier1	ENSG00000151576	55	0	0	48	23	32.39
1019	KDM6A	p.R1118P	X	44942752	44942752 G	C	SNP	tier1	ENSG00000147050	405	0	0	487	32	6.17
1021	SF3B1	p.K666N	2	198267359	198267359 C	G	SNP	tier1	ENSG00000115524	205	3	1.44	156	118	42.91
1021	ENSG00000183298	NULL	1	102252598	102252598 G	A	SNP	tier3	ENSG00000183298	55	0	0	24	25	51.02
1021	VAV3	p.N49S	1	108507346	108507346 T	C	SNP	tier1	ENSG00000134215	61	3	4.55	47	22	31.88
1021	WT1	p.S381fs	11	32417910	32417911 -	ACCGTACA	INS	tier1	ENSG00000184937	205	2	0.97	160	41	20.4
1021	ATM	p.R1730*	11	108172385	108172385 C	T	SNP	tier1	ENSG00000149311	50	0	0	72	6	7.69
1021	SPATA22	e7+7	17	3346461	3346461 T	A	SNP	tier2	ENSG00000141255	72	0	0	74	4	5.13
1021	RBFOX3	NULL	17	77086561	77086561 C	T	SNP	tier2	ENSG00000167281	98	2	2	52	39	42.86
1021	NOL4	p.R468W	18	31537316	31537316 G	A	SNP	tier1	ENSG00000101746	60	0	0	51	14	21.21
1021	CYP2D7P1	p.P474L	22	42536359	42536359 G	A	SNP	tier1	ENSG00000205702	147	1	0.68	106	40	27.21
1021	MAGI1	NULL	3	65341725	65341725 A	-	DEL	tier2	ENSG00000151276	131	0	0	108	0	0
1021	KIT	p.C97F	4	55561900	55561900 G	T	SNP	tier1	ENSG00000157404	279	0	0	287	8	2.69
1021	KIT	p.D816V	4	55599321	55599321 A	T	SNP	tier1	ENSG00000157404	141	3	2.08	100	59	36.88
1021	NRG2	e7+24	5	139241310	139241310 G	A	SNP	tier3	ENSG00000158458	61	1	1.61	22	20	47.62
1021	NPM1	p.W288fs	5	170837543	170837544 -	TCTG	INS	tier1	ENSG00000181163	178	1	0.56	140	75	34.88
1021	CCND3	p.P284L	6	41903706	41903706 G	A	SNP	tier1	ENSG00000112576	90	0	0	120	0	0
1021	FAM126A	p.R229K	7	23004091	23004091 C	T	SNP	tier1	ENSG00000122591	99	7	6.6	52	29	35.8
1021	NUP188	p.R1704Q	9	131768818	131768818 G	A	SNP	tier1	ENSG00000095319	67	0	0	77	1	1.28
1021	EDA	e2+1482	X	69178464	69178464 G	T	SNP	tier3	ENSG00000158813	68	1	1.45	16	58	78.38
1021	TAF7L	e7-4	X	100534027	100534027 T	C	SNP	tier3	ENSG00000102387	47	3	6	17	42	71.19
1021	OR13H1	p.A2S	X	130678051	130678051 G	T	SNP	tier1	ENSG0000017054	122	1	0.81	22	100	81.97
1022	IDH1	p.R132C	2	209113113	209113113 G	A	SNP	tier1	ENSG00000138413	590	0	0	163	87	34.8
1022	CLCA2	NULL	1	86873971	86873971 C	T	SNP	tier3	ENSG00000137975	147	2	1.34	36	10	21.28
1022	SPTA1	p.G559R	1	158639501	158639501 C	T	SNP	tier1	ENSG00000163554	147	0	0	32	5	13.51
1022	DNM3	e14-151	1	172062685	172062685 T	C	SNP	tier3	ENSG00000197959	124	0	0	32	18	36
1022	CFH	p.W379C	1	196658722	196658722 G	T	SNP	tier1	ENSG0000000971	103	0	0	28	6	17.65
1022	TRIM3	p.N670S	11	6470609	6470609 T	C	SNP	tier1	ENSG00000110171	144	1	0.69	16	15	48.39
1022	BIRC2	p.K94fs	11	102220865	102220866 -	GTTCC	INS	tier1	ENSG00000110330	122	0	0	45	3	6.25

1022	SLCO1B3	e3-27	12	21011346	21011346 A	G	SNP	tier2	ENSG00000111700	130	0	0	29	26	47.27
1022	KCNC2	p.R300C	12	75444887	75444887 G	A	SNP	tier1	ENSG00000166006	215	0	0	64	24	27.27
1022	DZIP1	e3+9	13	96285479	96285479 A	G	SNP	tier3	ENSG00000134874	149	0	0	23	9	28.12
1022	HIF1A	e14-2	14	62212402	62212407 TTTATA	-	DEL	tier1	ENSG00000100644	109	0	0	26	14	35
1022	ATXN3	p.Q63H	14	92563018	92563018 C	G	SNP	tier1	ENSG00000066427	52	0	0	10	1	9.09
1022	AK7	p.I536R	14	96944853	96944853 T	G	SNP	tier1	ENSG00000140057	110	0	0	29	20	40.82
1022	HERC1	p.Y3033C	15	63954024	63954024 T	C	SNP	tier1	ENSG00000103657	118	0	0	17	11	39.29
1022	WRAP53	p.Q482	17	7606603	7606603 G	A	SNP	tier1	ENSG00000141499	83	0	0	33	0	0
1022	CELF4	p.M254V	18	34854315	34854315 T	C	SNP	tier1	ENSG00000101489	104	0	0	26	0	0
1022	CEACAM21	e6-72	19	42092121	42092121 C	T	SNP	tier3	ENSG00000007129	45	30	40	9	3	25
1022	DNMT3A	p.E856K	2	25458607	25458607 C	T	SNP	tier1	ENSG00000119772	518	0	0	121	68	35.98
1022	NBEAL1	e49-33	2	204067377	204067377 G	C	SNP	tier3	ENSG00000144426	44	30	40.54	19	12	38.71
1022	TPTE	e21-168	21	10907208	10907208 C	A	SNP	tier3	ENSG00000166157	167	34	16.83	64	21	24.71
1022	SH3BGR	e5+37	21	40880991	40880991 G	A	SNP	tier3	ENSG00000185437	84	0	0	16	7	30.43
1022	POPD2	p.V87	3	119379010	119379010 G	T	SNP	tier1	ENSG00000121577	88	0	0	18	0	0
1022	SLC9A9	e6-7919	3	143379121	143379121 G	T	SNP	tier4	ENSG00000181804	122	0	0	28	0	0
1022	HERC6	p.Q645*	4	89345852	89345852 C	T	SNP	tier1	ENSG00000138642	82	0	0	29	0	0
1022	CHD1	p.N487fs	5	98232929	98232929 A	-	DEL	tier1	ENSG00000153922	117	0	0	31	7	18.42
1022	CHD1	p.L486	5	98232932	98232932 C	T	SNP	tier1	ENSG00000153922	117	0	0	31	7	18.42
1022	CHD1	p.L485fs	5	98232934	98232935 -	AGGGC	INS	tier1	ENSG00000153922	120	0	0	33	6	15.38
1022	PCDH86	p.S470	5	140531248	140531248 C	T	SNP	tier1	ENSG00000113211	499	16	3.11	200	4	1.96
1022	AMD1	NULL	6	111215478	111215478 G	A	SNP	tier3	ENSG00000123505	88	0	0	19	5	20.83
1022	NCOA7	p.G119V	6	126199413	126199413 G	T	SNP	tier1	ENSG00000111912	115	0	0	39	0	0
1022	ENSG00000226943	NULL	7	6969326	6969326 C	A	SNP	tier3	ENSG00000226943	220	0	0	45	0	0
1022	PION	p.T323N	7	76990200	76990200 G	T	SNP	tier1	ENSG00000186088	125	0	0	25	0	0
1022	TPM2	e2-31	9	35689299	35689299 T	C	SNP	tier2	ENSG00000198467	128	0	0	22	10	31.25
1022	TTL11	e8+66	9	124622550	124622550 C	A	SNP	tier3	ENSG00000175764	146	0	0	37	20	35.09
1022	UBAC1	e9+49	9	138830019	138830019 C	T	SNP	tier3	ENSG00000130560	101	0	0	31	1	3.12
1022	CNKS2	p.S503G	X	21581469	21581469 A	G	SNP	tier1	ENSG00000149970	172	0	0	46	0	0
1022	ENSG00000196395	NULL	X	52857169	52857169 C	T	SNP	tier3	ENSG00000196395	234	0	0	33	16	32.65
1023	TP53	p.R273C	17	7577121	7577121 G	A	SNP	tier1	ENSG00000141510	123	0	0	22	79	77.45
1023	USP24	e17+60	1	55614076	55614076 T	A	SNP	tier3	ENSG00000162402	84	0	0	60	42	41.18
1023	CTGLF10P	NULL	10	46174373	46174373 T	G	SNP	tier3	ENSG00000230869	183	0	0	207	2	0.96
1023	TECTB	p.V102I	10	114045865	114045865 G	A	SNP	tier1	ENSG00000119913	89	0	0	26	23	46.94
1023	MED13L	NULL	12	116397088	116397088 A	T	SNP	tier3	ENSG00000123066	143	0	0	198	1	0.5
1023	DGKZP1	NULL	13	44543629	44543629 C	T	SNP	tier2	ENSG00000179611	53	1	1.85	37	0	0
1023	RRN3P2	NULL	16	29110458	29110458 T	C	SNP	tier3	ENSG00000103472	83	0	0	80	7	7.95
1023	FBXW10	p.V1027A	17	18682505	18682505 T	C	SNP	tier1	ENSG00000171931	120	5	4	9	7	43.75
1023	KRT36	p.R112C	17	39645783	39645783 G	A	SNP	tier1	ENSG00000126337	103	1	0.96	40	38	48.1
1023	ENSG00000205334	p.G185S	2	27930480	27930480 C	T	SNP	tier1	ENSG00000205334	68	0	0	58	40	40.4
1023	FABP1	e1+31	2	88427439	88427439 C	T	SNP	tier2	ENSG00000163586	52	0	0	25	23	47.92
1023	TEKT4	p.R424C	2	95542476	95542476 C	T	SNP	tier1	ENSG00000163060	86	1	1.15	62	10	13.89
1023	LAMA2	p.N571	6	129513929	129513929 C	T	SNP	tier1	ENSG00000196569	81	0	0	59	0	0
1023	ZCCHC7	p.I75	9	37126554	37126554 C	T	SNP	tier1	ENSG00000147905	56	0	0	29	14	32.56
					GGATCTGCACA										
					TTC CATT TCTTAC										
					CAA ACTCTAA										
					TTTTCTCTTGA										
					AACTCCATT										
					GAGATCATATT										
					CAT ATTCTCTG										
1024	FLT3	ITD	13	28608276	28608277 -	AA	INS	tier1	ENSG00000122025	227	0	0	261	6	3
1024	MIR371A	NULL	19	54260132	54260132 C	T	SNP	tier3	ENSG00000199031	57	0	0	34	21	38.18
1024	CAPN13	e13+22	2	30965170	30965170 C	T	SNP	tier2	ENSG00000162949	87	3	3.33	35	33	47.14
1024	RSRC1	e3+22374	3	157943408	157943408 A	G	SNP	tier3	ENSG00000174891	49	1	2	38	27	41.54
1024	NPM1	p.W287fs	5	170837545	170837546 -	TGCA	INS	tier1	ENSG00000181163	185	8	4.15	115	49	29.88

1024	COL12A1	p.G839R	6	75884949	75884949 C	T	SNP	tier1	ENSG00000111799	325	13	3.85	186	138	42.46
1024	JAK2	e7-82	9	5064801	5064801 C	T	SNP	tier2	ENSG0000096968	84	4	4.55	55	34	37.78
1025	U2AF1	p.S34Y	21	44524456	44524456 G	T	SNP	tier1	ENSG00000160201	440	11	2.44	220	174	44.16
1025	ETV6	p.S131fs	12	12006417	12006418 -	T	INS	tier1	ENSG00000139083	465	7	1.48	222	164	42.49
1025	DGKZP1	NULL	13	44545383	44545383 C	T	SNP	tier2	ENSG00000179611	54	1	1.82	27	12	30.77
1025	PPARA	p.R128Q	22	46614173	46614173 G	A	SNP	tier1	ENSG00000186951	53	0	0	38	19	33.33
1025	OTOL1	p.S404R	3	161221508	161221508 T	G	SNP	tier1	ENSG00000182447	77	0	0	35	15	30
1025	LMLN	NULL	3	197770578	197770578 A	G	SNP	tier2	ENSG00000185621	62	1	1.59	38	12	24
1025	ODZ3	p.R813W	4	183650186	183650186 C	T	SNP	tier1	ENSG00000218336	57	0	0	17	22	56.41
1027	IDH2	p.R172K	15	90631838	90631838 C	T	SNP	tier1	ENSG00000182054	192	3	1.54	158	136	46.26
1027	DNMT3A	p.R882H	2	25457242	25457242 C	T	SNP	tier1	ENSG00000119772	87	3	3.33	14	158	91.33
1027	ESPNP	NULL	1	17034456	17034463 GCGCGCTT	-	DEL	tier2	ENSG00000116219	70	2	2.78	86	3	3.37
1027	ENSG00000233515	NULL	10	43221241	43221241 C	T	SNP	tier3	ENSG00000233515	75	0	0	62	43	40.95
1027	C10orf28	p.S307P	10	99968790	99968790 T	C	SNP	tier1	ENSG00000166024	204	2	0.97	95	140	59.57
1027	ENSG00000260781	NULL	16	33730849	33730849 G	A	SNP	tier2	ENSG00000260781	96	0	0	82	35	29.66
1027	ENSG00000260781	NULL	16	33738995	33738995 C	T	SNP	tier3	ENSG00000260781	77	0	0	64	28	30.11
1027	GCGR	p.L252	17	79769623	79769623 C	T	SNP	tier1	ENSG00000215644	68	0	0	29	29	50
CCCGGAGCTCC															
1027	KIR2DS4	p.l152fs	19	55350963	55350964 -	TATGACATGTA	INS	tier1	ENSG00000221957	79	2	2.47	95	14	12.84
1027	ATP2B2	NULL	3	10367943	10367944 GT	-	DEL	tier4	ENSG00000157087	78	0	0	105	1	0.94
1027	CEP63	p.A505T	3	134277029	134277029 G	A	SNP	tier1	ENSG00000182923	58	0	0	34	25	42.37
1027	FAM90A2P	NULL	8	12030358	12030358 C	G	SNP	tier3	ENSG00000205879	80	1	1.23	40	10	20
1027	SH3KBP1	p.T593	X	19560156	19560156 C	T	SNP	tier1	ENSG00000147010	65	0	0	44	42	48.84
1027	BCOR	p.N574fs	X	39932876	39932877 -	G	INS	tier1	ENSG00000183337	166	2	1.19	101	69	40.59
1028	KRAS	p.A146V	12	25378561	25378561 G	A	SNP	tier1	ENSG00000133703	469	1	0.21	608	40	6.16
1028	KRAS	p.G12R	12	25398285	25398285 C	G	SNP	tier1	ENSG00000133703	449	1	0.22	441	16	3.5
1028	IDH2	p.R140Q	15	90631934	90631934 C	T	SNP	tier1	ENSG00000182054	399	16	3.86	320	276	46.23
1028	FAT3	p.A3348	11	92568208	92568208 G	A	SNP	tier1	ENSG00000165323	77	3	3.75	36	27	42.86
1028	MUC19	NULL	12	40916528	40916528 C	G	SNP	tier3	ENSG00000205592	80	0	0	75	9	10.71
1028	SRSF2	p.P95R	17	74732959	74732959 G	C	SNP	tier1	ENSG00000161547	202	8	3.79	200	150	42.86
1028	UNC80	p.C929F	2	210698736	210698736 G	T	SNP	tier1	ENSG00000144406	68	4	5.56	30	30	50
1028	C21orf67	p.S127N	21	46354971	46354971 C	T	SNP	tier1	ENSG00000183250	61	0	0	95	13	11.93
1028	FREM3	p.H659	4	144619852	144619852 A	G	SNP	tier1	ENSG00000183090	65	2	2.99	50	25	33.33
1028	SHROOM2	p.P1232	X	9905282	9905282 C	T	SNP	tier1	ENSG00000146950	281	0	0	350	19	5.15
1035	IDH2	p.R140Q	15	90631934	90631934 C	T	SNP	tier1	ENSG00000182054	105	0	0	217	20	8.4
1035	GBP3	p.T585fs	1	89473441	89473442 -	T	INS	tier1	ENSG00000117226	72	0	0	93	10	9.71
1035	ASPM	NULL	1	197125495	197125495 C	T	SNP	tier3	ENSG00000066279	87	3	3.33	185	22	10.58
1035	MUC5B	p.G4152	11	1270557	1270557 C	T	SNP	tier1	ENSG00000117983	164	3	1.8	190	24	11.21
1035	PRR5L	p.Q57H	11	36424854	36424854 G	T	SNP	tier1	ENSG00000135362	57	0	0	45	4	8.16
1035	PARPBP	p.T225M	12	102559514	102559514 C	T	SNP	tier1	ENSG00000185480	65	0	0	90	0	0
1035	OR1D2	p.L32	17	2996197	2996197 G	A	SNP	tier1	ENSG00000184166	56	3	5.08	75	11	12.79
1035	SRSF2	p.P95H	17	74732959	74732959 G	T	SNP	tier1	ENSG00000161547	54	0	0	80	9	10.11
1035	ENSG00000233087	NULL	2	132119324	132119324 T	C	SNP	tier3	ENSG00000233087	82	1	1.2	122	16	11.59
CACCACTGCCA															
1035	ASXL1	p.H633fs	20	31022403	31022425 TAGAGAGCGC	-	DEL	tier1	ENSG00000171456	180	0	0	294	11	3.61
1035	SLT2	e6+48	4	20482458	20482458 G	T	SNP	tier3	ENSG00000145147	53	1	1.85	56	8	12.5
1035	DAPK1	NULL	9	90323421	90323422 TA	-	DEL	tier4	ENSG00000196730	64	0	0	80	1	1.23
1035	EHMT1	p.Y296H	9	140637885	140637885 T	C	SNP	tier1	ENSG00000181090	73	5	6.41	103	10	8.85
1035	KDM5C	e9-5	X	53241093	53241093 A	C	SNP	tier3	ENSG00000126012	62	1	1.59	93	2	2.11
1035	DACH2	p.E67K	X	85403823	85403823 G	A	SNP	tier1	ENSG00000126733	57	0	0	62	3	4.41
1035	PABPC5	NULL	X	90692423	90692423 T	C	SNP	tier4	ENSG00000174740	64	1	1.54	91	7	7.14
1036	IDH1	p.R132C	2	209113113	209113113 G	A	SNP	tier1	ENSG00000138413	357	1	0.28	475	72	13.16
1036	CRB1	p.G833C	1	197396952	197396952 G	T	SNP	tier1	ENSG00000134376	50	1	1.92	52	19	26.76
1036	HDAC7	p.R361	12	48189425	48189425 G	C	SNP	tier1	ENSG0000061273	88	0	0	65	16	19.75
1036	PACS2	p.S547Y	14	105849710	105849710 C	A	SNP	tier1	ENSG00000179364	50	1	1.96	33	11	25

1036	RUNX1	e7-1	21	36171760	36171760 C	T	SNP	tier1	ENSG00000159216	547	0	0	592	0	0
1036	CD47	NULL	3	107762156	107762156 T	A	SNP	tier2	ENSG00000196776	191	3	1.55	166	55	24.89
1036	BBS7	p.T318P	4	122768644	122768644 T	G	SNP	tier1	ENSG00000138686	61	0	0	57	20	25.97
1036	CCHCR1	p.E703K	6	31112524	31112524 C	T	SNP	tier1	ENSG00000204536	66	1	1.49	46	21	31.34
1036	FAM22G	NULL	9	99691302	99691302 A	T	SNP	tier3	ENSG00000188152	66	0	0	111	33	22.92
1040	IDH2	p.R140Q	15	90631934	90631934 C	T	SNP	tier1	ENSG00000182054	211	0	0	279	7	2.45
1040	KIAA1462	p.S300	10	30318177	30318177 C	T	SNP	tier1	ENSG00000165757	64	0	0	66	18	21.43
1040	EP400	e23-31	12	132505593	132505593 G	A	SNP	tier2	ENSG00000183495	66	0	0	61	19	23.75
1040	TP53TG3	NULL	16	32266116	32266117 -	TACTT	INS	tier3	ENSG00000205456	158	0	0	185	7	3.65
1040	AP1G1	p.C8	16	71842712	71842712 G	A	SNP	tier1	ENSG00000166747	89	0	0	112	5	4.27
1040	ENSG00000222463	NULL	18	4988109	4988109 G	A	SNP	tier1	ENSG00000222463	53	0	0	48	5	9.43
1040	EPB41L3	p.G42	18	5630515	5630515 T	C	SNP	tier1	ENSG00000082397	82	0	0	68	9	11.69
1040	OSBPL6	p.P361	2	179214034	179214034 C	G	SNP	tier1	ENSG00000079156	65	0	0	55	0	0
1040	TUBGCP6	p.P241L	22	50665428	50665428 G	A	SNP	tier1	ENSG00000128159	64	0	0	42	17	28.81
1040	LOC100129931	NULL	4	7034815	7034815 T	G	SNP	tier2	ENSG00000245748	84	0	0	75	15	16.67
1040	NSUN7	p.S77C	4	40752940	40752940 C	G	SNP	tier1	ENSG00000179299	51	0	0	59	4	6.35
1040	TET2	p.H578fs	4	106156829	106156829 C	-	DEL	tier1	ENSG00000168769	279	1	0.36	287	25	8.01
1040	TET2	p.H1380Q	4	106190862	106190862 T	A	SNP	tier1	ENSG00000168769	91	0	0	129	9	6.52
1040	ITGA2	NULL	5	52389728	52389728 A	G	SNP	tier3	ENSG00000164171	66	1	1.49	55	4	6.78
1040	NPM1	p.W288fs	5	170837543	170837544 -	TCTG	INS	tier1	ENSG00000181163	182	0	0	172	7	3.91
1040	FAM153C	p.A63T	5	177468747	177468747 G	A	SNP	tier1	ENSG00000204677	112	0	0	127	6	4.51
1040	RIMS1	e26-41	6	73001596	73001596 G	A	SNP	tier3	ENSG00000079841	145	0	0	142	2	1.39
1040	L3MBTL3	p.I316F	6	130387579	130387579 A	T	SNP	tier1	ENSG00000198945	121	0	0	105	33	23.91
1040	PEX1	NULL	7	92131201	92131201 T	C	SNP	tier3	ENSG00000127980	78	1	1.27	83	6	6.74
1040	GTPBP6	p.V269M	X	221800	221800 C	T	SNP	tier1	ENSG00000178605	56	0	0	43	13	23.21
1040	FAM47A	p.S570L	X	34148687	34148687 G	A	SNP	tier1	ENSG00000185448	375	0	0	398	11	2.69
1041	TET2	p.C484fs	4	106156548	106156548 T	-	DEL	tier1	ENSG00000168769	173	2	1.14	127	61	32.45
1041	DNAH5	p.A680	5	13901373	13901373 C	T	SNP	tier1	ENSG00000039139	164	3	1.8	112	98	46.67
1041	ENSG00000223566	NULL	7	63032656	63032656 G	A	SNP	tier2	ENSG00000223566	66	0	0	68	22	24.44
1041	PHF6	e5+2	X	133547689	133547689 T	C	SNP	tier1	ENSG00000156531	63	4	5.97	10	92	90.2
1042	GATA2	p.R398W	3	128200113	128200113 G	A	SNP	tier1	ENSG00000179348	143	0	0	138	2	1.43
1042	IPO9	e8+55	1	201824106	201824106 G	A	SNP	tier3	ENSG00000198700	52	0	0	49	43	46.74
1042	MRGPRX4	NULL	11	18194714	18194714 C	T	SNP	tier4	ENSG00000179817	51	0	0	40	22	35.48
1042	PTTE2P3	NULL	13	53073452	53073452 A	G	SNP	tier3	ENSG00000198384	72	0	0	49	47	48.96
1042	RBFOX1	NULL	16	7762199	7762199 G	A	SNP	tier2	ENSG00000078328	68	0	0	46	32	41.03
1042	SRSF2	p.P95L	17	74732959	74732959 G	A	SNP	tier1	ENSG00000161547	109	0	0	73	73	50
1042	SETBP1	p.G870S	18	42531913	42531913 G	A	SNP	tier1	ENSG00000152217	230	0	0	226	40	15.04
1042	FCGBP	p.D4196G	19	40368761	40368761 T	C	SNP	tier1	ENSG00000090920	668	0	0	660	143	17.81
1042	LILRA1	e3+4	19	55106421	55106421 A	G	SNP	tier3	ENSG00000104974	75	0	0	48	32	40
1042	DNAH7	e1+77	2	196933344	196933344 G	A	SNP	tier2	ENSG00000118997	69	0	0	45	32	41.56
1042	TNS1	e1+57	2	218867506	218867506 G	A	SNP	tier3	ENSG00000079308	78	0	0	77	2	2.47
1042	ASXL1	p.Q588*	20	31022277	31022277 C	T	SNP	tier1	ENSG00000171456	378	1	0.26	37	207	84.84
1042	EXOG	p.N176K	3	38545180	38545180 C	G	SNP	tier1	ENSG00000157036	67	0	0	61	35	36.08
1042	NIPAL1	p.T47	4	48027179	48027179 G	A	SNP	tier1	ENSG00000163293	60	0	0	28	30	50.85
1042	OFCC1	p.A215fs	6	9900627	9900627 C	-	DEL	tier1	ENSG00000181355	67	0	0	42	31	42.47
1042	MCART3P	NULL	6	66499083	66499083 A	G	SNP	tier3	ENSG00000220483	96	0	0	125	0	0
1042	MLL5	e7-25	7	104716465	104716465 A	G	SNP	tier3	ENSG0000005483	71	0	0	115	16	12.21
1042	WDR60	e2-343	7	158662203	158662203 T	C	SNP	tier4	ENSG00000126870	82	0	0	77	8	9.41
1042	BCOR	e9+1	X	39921391	39921391 C	A	SNP	tier1	ENSG00000183337	73	0	0	70	21	23.08
1042	STAG2	p.W495*	X	123195141	123195141 G	A	SNP	tier1	ENSG00000101972	98	0	0	55	83	60.14
1043	IDH2	p.R172K	15	90631838	90631838 C	T	SNP	tier1	ENSG00000182054	331	0	0	335	12	3.46
1043	FLG2	p.G1484E	1	152325811	152325811 C	T	SNP	tier1	ENSG00000143520	96	0	0	78	4	4.88
						GAAGTTAAAT									
1043	LIN7C	e3-51	11	27523164	27523165 -	TTCAGGC	INS	tier3	ENSG00000148943	54	1	1.82	53	13	19.7
1043	WT1	p.R458P	11	32413577	32413577 C	G	SNP	tier1	ENSG00000184937	183	0	0	188	6	3.09
1043	MED12	p.F441V	X	70342430	70342430 T	G	SNP	tier1	ENSG00000184634	284	0	0	266	12	4.29

1044	NRAS	p.G13R	1	115258745	115258745 C	G	SNP	tier1	ENSG00000213281	205	0	0	216	71	24.65
1044	U2AF1	p.Q157P	21	44514777	44514777 T	G	SNP	tier1	ENSG00000160201	132	2	1.49	114	93	44.93
1044	PRAMEF14	p.R434W	1	13669030	13669030 G	A	SNP	tier1	ENSG00000204481	56	2	3.45	48	32	40
1044	ENSG00000227141	NULL	1	179557882	179557882 C	T	SNP	tier3	ENSG00000227141	56	0	0	47	23	32.86
1044	ETV6	p.H180fs	12	12022430	12022431 -	A	INS	tier1	ENSG00000139083	267	4	1.48	183	138	42.99
1044	MTHFD1	e7-87	14	64884519	64884519 G	A	SNP	tier3	ENSG00000100714	68	0	0	40	29	42.03
1044	STX8	e7+7659	17	9274210	9274210 A	C	SNP	tier2	ENSG00000170310	90	0	0	99	37	27.21
1044	MIR142	NULL	17	56408647	56408647 A	G	SNP	tier1	ENSG00000207567	118	1	0.84	89	63	41.45
1044	MIR142	NULL	17	56408648	56408648 G	C	SNP	tier1	ENSG00000207567	118	1	0.84	89	65	42.21
				CACCACTGCCA											
1044	ASXL1	p.H633fs	20	31022403	31022425 TAGAGAGGCG	-	DEL	tier1	ENSG00000171456	388	2	0.51	379	56	12.87
1044	CADM2	e2-290255	3	85560942	85560942 C	T	SNP	tier3	ENSG00000175161	50	0	0	53	10	15.87
1044	GATA2	e_del	3	128200135	128200140 CTTCTT	-	DEL	tier1	ENSG00000179348	148	2	1.33	135	32	19.16
1044	UGT8	NULL	4	115604691	115604691 G	A	SNP	tier3	ENSG00000174607	75	6	7.41	54	33	37.93
1044	MEGF10	e1+74	5	126667190	126667190 G	A	SNP	tier3	ENSG00000145794	55	2	3.51	34	30	46.88
1044	PCDHB10	p.A600P	5	140573923	140573923 G	C	SNP	tier1	ENSG00000120324	73	1	1.35	37	28	43.08
1044	TDH	NULL	8	11223153	11223153 C	T	SNP	tier3	ENSG00000154316	58	3	4.92	37	38	50.67
1044	FAM75C2	NULL	9	90748620	90748620 C	G	SNP	tier3	ENSG00000177910	76	1	1.28	63	44	41.12
1045	ENSG00000222787	NULL	1	30357844	30357844 C	T	SNP	tier1	ENSG00000222787	68	1	1.45	47	26	35.62
1045	TNN	p.D629N	1	175067497	175067497 G	A	SNP	tier1	ENSG00000120332	69	0	0	44	26	37.14
1045	CHD4	p.R1340H	12	6692405	6692405 C	T	SNP	tier1	ENSG00000111642	238	3	1.24	173	130	42.76
1045	ATPSB	p.G3V	12	57039740	57039740 C	A	SNP	tier1	ENSG00000110955	53	0	0	40	24	37.5
1045	DNAH10	p.T1903M	12	124333389	124333389 C	T	SNP	tier1	ENSG00000197653	74	0	0	37	42	53.16
1045	CCDC168	p.E1281	13	103385317	103385317 C	T	SNP	tier1	ENSG00000175820	60	0	0	35	38	52.05
1045	ENSG00000206906	NULL	14	19123723	19123723 A	G	SNP	tier2	ENSG00000206906	199	2	1	206	55	21.07
1045	RPL7AP6	NULL	14	70352127	70352127 G	A	SNP	tier3	ENSG00000242071	80	0	0	52	39	42.86
1045	NRXN3	p.Y674	14	79181460	79181460 C	T	SNP	tier1	ENSG00000021645	152	0	0	190	1	0.52
1045	CLEC18B	NULL	16	74445531	74445531 C	G	SNP	tier3	ENSG00000140839	269	1	0.37	316	52	14.09
1045	PRPF8	p.D1598N	17	1563289	1563289 C	T	SNP	tier1	ENSG00000174231	212	3	1.4	186	128	40.76
1045	CALR	p.D118	19	13050402	13050402 C	T	SNP	tier1	ENSG00000179218	225	0	0	358	4	1.1
1045	APOB	p.R427*	2	21255299	21255299 G	A	SNP	tier1	ENSG00000084674	177	0	0	231	1	0.43
1045	KCNIP3	NULL	2	96051249	96051249 G	A	SNP	tier2	ENSG00000115041	54	1	1.82	33	30	47.62
1045	GRCPD1	NULL	20	5565468	5565468 G	C	SNP	tier3	ENSG00000125772	60	1	1.64	28	29	50.88
1045	DNAH5	p.L2488	5	13810313	13810313 C	T	SNP	tier1	ENSG00000039139	179	3	1.65	143	86	37.55
1045	NPM1	p.W288fs	5	170837543	170837544 -	TCTG	INS	tier1	ENSG00000181163	225	1	0.44	217	109	33.44
1045	SCARA5	p.R43W	8	27824045	27824045 G	A	SNP	tier1	ENSG00000168079	62	1	1.59	44	29	39.73
1045	KCNU1	e26+14	8	36790564	36790564 A	T	SNP	tier3	ENSG00000215262	192	0	0	267	2	0.74
1045	PHF6	p.Y304N	X	133551271	133551271 T	A	SNP	tier1	ENSG00000156531	133	4	2.92	42	149	78.01
1049	SF3B1	p.K700E	2	198266834	198266834 T	C	SNP	tier1	ENSG00000115524	202	6	2.88	237	60	20.13
1049	IDH1	p.R132C	2	209113113	209113113 G	A	SNP	tier1	ENSG00000138413	339	0	0	364	32	8.08
1049	EPHB2	p.M816I	1	23235610	23235610 G	A	SNP	tier1	ENSG00000133216	96	1	1.03	105	17	13.93
1049	PCSK9	p.A53D	1	55505668	55505668 G	A	SNP	tier1	ENSG00000169174	65	0	0	71	5	6.58
1049	POGZ	NULL	1	151375467	151375467 G	T	SNP	tier3	ENSG00000143442	58	0	0	50	9	15.25
1049	SORCS1	e23+102	10	108366822	108366822 T	C	SNP	tier3	ENSG00000108018	54	3	5.26	61	9	12.86
1049	SLC37A2	p.L28Q	11	124946676	124946676 T	A	SNP	tier1	ENSG00000134955	69	0	0	44	0	0
1049	RIMBP2	p.N523	12	130922946	130922946 G	A	SNP	tier1	ENSG00000060709	115	0	0	94	13	12.15
1049	SKA3	p.R396S	13	21729882	21729882 C	A	SNP	tier1	ENSG00000165480	85	0	0	124	11	8.15
1049	NRXN3	p.T1275M	14	80164180	80164180 C	T	SNP	tier1	ENSG00000021645	665	0	0	589	21	3.44
1049	UBE2F	NULL	2	238841537	238841537 C	T	SNP	tier4	ENSG00000184182	83	0	0	83	4	4.55
1049	COL20A1	e20+34	20	61948077	61948077 C	T	SNP	tier3	ENSG00000101203	54	0	0	48	11	18.64
1049	KCNQ2	p.A833V	20	62038142	62038142 G	A	SNP	tier1	ENSG00000075043	356	0	0	451	22	4.65
1049	CHEK2	p.R517C	22	29090061	29090061 G	A	SNP	tier1	ENSG00000183765	99	0	0	119	18	13.14
1049	CMAHP	p.R296*	6	25097341	25097341 G	A	SNP	tier1	ENSG00000168405	99	0	0	89	8	8.25
1049	PNR1C	p.S291N	6	89793803	89793803 G	A	SNP	tier1	ENSG00000146278	65	0	0	57	3	5
1049	RIMS2	e13-44	8	104943447	104943447 G	A	SNP	tier3	ENSG00000176406	84	2	2.33	72	20	21.74

1049	WNK3	NULL	X	54223753	54223753 A	G	SNP	tier3	ENSG00000196632	56	0	0	65	10	13.33
1050	IDH2	p.R172K	15	90631838	90631838 C	T	SNP	tier1	ENSG00000182054	327	0	0	569	4	0.7
1050	IDH1	p.R132C	2	209113113	209113113 G	A	SNP	tier1	ENSG00000138413	235	1	0.42	420	5	1.18
1050	CYP4Z1	e4-64	1	47547942	47547942 G	A	SNP	tier3	ENSG00000186160	54	1	1.79	41	16	28.07
1050	PM20D1	p.A406V	1	205801794	205801794 G	A	SNP	tier1	ENSG00000162877	120	0	0	124	46	27.06
1050	ATP11A	NULL	13	113538580	113538580 C	A	SNP	tier2	ENSG00000068650	57	1	1.72	53	18	25
1050	GOLGA6L2	e3-3	15	23689650	23689650 G	A	SNP	tier2	ENSG00000174450	78	0	0	81	23	22.12
1050	ENSG00000226145	NULL	17	16723414	16723414 C	T	SNP	tier1	ENSG00000226145	101	0	0	104	22	17.46
1050	RUNX1	p.E422*	21	36164611	36164611 C	A	SNP	tier1	ENSG00000159216	351	0	0	243	114	31.84
						GGGCACAGGC									
1050	TPPP	e2-6	5	666244	666245 -	GACTTA	INS	tier3	ENSG00000171368	73	3	3.95	72	7	8.86
1050	ANKH	e10-31	5	14713807	14713807 G	A	SNP	tier3	ENSG00000154122	50	0	0	50	16	24.24
1050	HNRNPA0	NULL	5	137087708	137087709 -	T	INS	tier2	ENSG00000177733	78	0	0	79	25	24.04
1050	HNRNPA0	NULL	5	137087709	137087709 A	T	SNP	tier2	ENSG00000177733	76	0	0	78	26	25
1050	LUC7L2	p.R312*	7	139094357	139094357 C	T	SNP	tier1	ENSG00000146963	55	0	0	55	18	24.66
						AAATAAAAAA									
1050	NSMAF	e12-17	8	59518611	59518612 -	T	INS	tier3	ENSG0000035681	87	2	2.25	69	10	12.66
1050	NTNG2	p.D136	9	135073547	135073547 C	T	SNP	tier1	ENSG00000196358	50	0	0	62	27	30.34
1050	H2BFM	e4-23	X	103295372	103295372 G	A	SNP	tier4	ENSG00000101812	128	0	0	136	10	6.85
1050	PHF6	p.Y241C	X	133547986	133547986 A	G	SNP	tier1	ENSG00000156531	251	0	0	276	104	27.3
1051	KRAS	p.G12D	12	25398284	25398284 C	T	SNP	tier1	ENSG00000133703	266	2	0.75	239	26	9.77
1051	CRYZ	p.V245I	1	75172678	75172678 C	T	SNP	tier1	ENSG00000116791	59	5	7.81	37	35	48.61
1051	ENSG00000219061	NULL	11	49860856	49860856 G	A	SNP	tier3	ENSG00000219061	164	14	7.87	111	68	37.99
1051	BRF1	NULL	14	105675825	105675825 G	A	SNP	tier3	ENSG00000185024	83	6	6.74	52	35	40.23
		p.110in_frame_i													
1051	IGHG4	nsPCP	14	106091681	106091682 -	TGGGCACGG	INS	tier1	ENSG00000211892	120	5	4	180	8	4.26
1051	MYO5B	p.S1494	18	47369740	47369740 C	T	SNP	tier1	ENSG00000167306	205	20	8.85	110	130	54.17
1051	MARK4	NULL	19	45742253	45742253 C	T	SNP	tier3	ENSG0000007047	68	3	4.23	53	38	41.76
1051	TTN	p.E5674K	2	179496982	179496982 C	T	SNP	tier1	ENSG00000155657	76	0	0	77	3	3.75
1051	CWC22	p.L599I	2	180817220	180817220 G	T	SNP	tier1	ENSG00000163510	63	3	4.55	49	32	39.51
1051	UNCSC	p.G116S	4	96256561	96256561 C	T	SNP	tier1	ENSG00000182168	53	0	0	55	0	0
1053	IDH2	p.R140Q	15	90631934	90631934 C	T	SNP	tier1	ENSG00000182054	193	0	0	194	104	34.78
1053	C1orf129	p.V129M	1	170934301	170934301 G	A	SNP	tier1	ENSG00000117501	57	0	0	68	26	27.66
1053	LRCH1	e19-7	13	47315770	47315770 G	A	SNP	tier3	ENSG00000136141	52	0	0	37	36	49.32
1053	IGHV3-30	e2-20	14	106791329	106791329 G	A	SNP	tier3	ENSG00000211953	87	1	1.14	76	22	22.45
1053	DNAH3	NULL	16	21030908	21030908 C	A	SNP	tier3	ENSG00000158486	51	0	0	37	33	47.14
1053	RNF212	p.A271V	4	1087237	1087237 G	A	SNP	tier1	ENSG00000178222	76	0	0	53	32	37.65
1053	SORBS2	NULL	4	186528484	186528484 G	T	SNP	tier3	ENSG00000154556	71	0	0	47	28	37.33
1053	KDM3B	p.M1570fs	5	137763725	137763726 -	TG	INS	tier1	ENSG00000120733	149	0	0	63	107	62.94
1053	SCRIB	e22-38	8	144886364	144886364 A	T	SNP	tier3	ENSG00000180900	55	0	0	40	28	41.18
1053	APBA1	p.A489	9	72082754	72082754 G	A	SNP	tier1	ENSG00000107282	50	0	0	30	14	31.82
1053	RBMB41	e6+15	X	106312470	106312470 G	T	SNP	tier2	ENSG00000089682	70	0	0	58	51	46.79
1053	MAGEA1	NULL	X	152511159	152511159 G	A	SNP	tier3	ENSG00000198681	84	0	0	75	61	44.85
1055	RUNX1	p.R162K	21	36252877	36252877 C	T	SNP	tier1	ENSG00000159216	441	22	4.75	113	296	72.37
1055	FPGT-TNNI3K	p.W757C	1	74905263	74905263 G	T	SNP	tier1	ENSG00000116783	65	2	2.99	26	37	58.73
1055	SYCP1	p.S83F	1	115400075	115400075 C	T	SNP	tier1	ENSG00000198765	102	0	0	66	23	25.84
1055	FMO2	p.H150	1	171165916	171165916 C	T	SNP	tier1	ENSG00000094963	74	4	5.13	29	28	49.12
1055	WDFY4	p.I2795F	10	50172046	50172046 A	T	SNP	tier1	ENSG00000128815	61	0	0	32	21	39.62
1055	ENSG00000219061	NULL	11	49855091	49855091 G	A	SNP	tier3	ENSG00000219061	140	11	7.28	58	58	50
1055	SETD1B	p.H8fs	12	122242657	122242657 -	C	INS	tier1	ENSG00000139718	78	1	1.27	41	24	36.92
1055	KIAA0564	e45-7	13	42142448	42142448 G	C	SNP	tier3	ENSG00000102763	56	1	1.72	36	32	47.06
1055	NALCN	p.Q627	13	101833572	101833572 C	T	SNP	tier1	ENSG00000102452	333	0	0	347	1	0.29
1055	NRXN3	p.P1510L	14	80327904	80327904 C	T	SNP	tier1	ENSG00000021645	522	8	1.51	215	232	51.9

CTGTGTCTCTC GCACAGTAATA CACGGCCCTGT																			
1055	IGHV4OR15-8	NULL	15	22472913	22472947 CC	-	DEL	tier2	ENSG00000259261	102	2	1.92	117	3	2.5				
1055	SLFN11	p.P897L	17	33679391	33679391 G	A	SNP	tier1	ENSG00000172716	65	3	4.41	32	17	34.69				
1055	CD300LD	p.L169	17	72576219	72576219 C	A	SNP	tier1	ENSG00000204345	53	1	1.85	31	22	41.51				
1055	SF3B1	p.E592K	2	198267705	198267705 C	T	SNP	tier1	ENSG00000115524	374	11	2.86	197	200	50.38				
1055	SF3B1	p.Q19E	2	198288672	198288672 G	C	SNP	tier1	ENSG00000115524	348	12	3.33	185	193	50.92				
1055	GIGYF2	e6+33	2	233626179	233626179 T	A	SNP	tier3	ENSG00000204120	184	0	0	145	35	19.44				
1055	ASXL1	p.R417*	20	31021250	31021250 C	T	SNP	tier1	ENSG00000171456	421	26	5.82	226	261	53.48				
1055	PRR23C	p.R190Q	3	138762894	138762894 C	T	SNP	tier1	ENSG00000233701	104	1	0.95	50	46	47.92				
1055	-	-	3	144163006	144163006 G	A	SNP	tier4	-	71	2	2.74	25	30	54.55				
1055	SI	p.L1612F	3	164712050	164712050 C	A	SNP	tier1	ENSG0000090402	376	0	0	285	0	0				
1055	KIT	p.D816V	4	55599321	55599321 A	T	SNP	tier1	ENSG00000157404	291	6	2.02	128	128	50				
1055	CMY45	p.R109Q	5	79024914	79024914 G	A	SNP	tier1	ENSG00000164309	504	15	2.89	202	227	52.79				
1055	DOCK2	p.K1226E	5	169468069	169468069 A	G	SNP	tier1	ENSG00000134516	254	11	4.15	106	111	51.15				
1055	DOPY1	p.M1869I	6	83855308	83855308 G	T	SNP	tier1	ENSG0000083097	78	3	3.7	31	21	40.38				
1055	SNAP91	e9+42	6	84326646	84326646 T	C	SNP	tier3	ENSG0000065609	93	1	1.06	34	27	44.26				
1055	RABGAP1	p.Q602R	9	125827637	125827637 A	G	SNP	tier1	ENSG0000011454	89	0	0	90	2	2.17				
1055	PDHA1	e12-61	X	19377546	19377546 C	G	SNP	tier3	ENSG00000131828	102	0	0	54	48	47.06				
1055	BCOR	p.S1642P	X	39913191	39913191 A	G	SNP	tier1	ENSG00000183337	452	4	0.88	269	201	42.68				
1058	TMEM167B	p.F13	1	109635540	109635540 T	C	SNP	tier1	ENSG00000215717	74	1	1.33	66	39	37.14				
1058	KIAA0040	NULL	1	175129491	175129492 TG	-	DEL	tier1	ENSG00000235750	58	0	0	51	1	1.92				
1058	NVL	e2-1	1	224514167	224514167 C	T	SNP	tier1	ENSG00000143748	61	0	0	39	34	46.58				
1058	OR2T3	p.N291K	1	248637524	248637524 C	A	SNP	tier1	ENSG00000196539	199	0	0	161	54	25.12				
1058	COL13A1	e9-19	10	71654289	71654289 G	T	SNP	tier3	ENSG00000197467	79	0	0	32	24	42.86				
1058	SMC3	p.R381Q	10	112343991	112343991 G	A	SNP	tier1	ENSG00000108055	406	0	0	442	19	4.12				
1058	TYR	p.A482S	11	89028388	89028388 G	T	SNP	tier1	ENSG0000077498	75	0	0	48	36	42.86				
1058	LDHB	p.S225N	12	21791326	21791326 C	T	SNP	tier1	ENSG00000111716	164	2	1.2	112	75	40.11				
1058	FRY	p.L762	13	32747638	32747638 A	G	SNP	tier1	ENSG0000073910	51	0	0	34	22	39.29				
1058	KLHL1	e6+7	13	70413101	70413101 T	C	SNP	tier3	ENSG00000150361	94	1	1.05	52	17	24.64				
1058	OR7C2	p.P129	19	15052687	15052687 C	G	SNP	tier1	ENSG00000127529	68	1	1.45	36	30	45.45				
1058	CEBPA	p.A303P	19	33792414	33792414 C	G	SNP	tier1	ENSG00000245848	274	5	1.79	159	118	42.6				
1058	SCTR	e8-1	2	120210924	120210924 C	A	SNP	tier1	ENSG0000080293	69	0	0	61	0	0				
1058	THSD7B	p.H1435P	2	138414650	138414650 A	C	SNP	tier1	ENSG00000144229	75	1	1.32	34	33	49.25				
1058	ABCG1	p.I759	21	43716304	43716304 C	A	SNP	tier1	ENSG00000160179	67	0	0	65	18	21.69				
1058	BCR	e2+633	22	23596800	23596800 G	A	SNP	tier3	ENSG00000186716	71	0	0	24	26	52				
1058	SF11	e8-1	22	31969043	31969043 G	A	SNP	tier1	ENSG00000198089	66	0	0	32	35	52.24				
1058	ENSG00000235805	NULL	3	44751791	44751791 C	T	SNP	tier3	ENSG00000235805	61	0	0	48	14	22.58				
1058	ATP13A4	p.Q148P	3	193210888	193210888 T	G	SNP	tier1	ENSG00000127249	63	0	0	50	23	31.51				
1058	TET2	p.Q1548*	4	106196309	106196309 C	T	SNP	tier1	ENSG00000168769	412	15	3.49	257	230	47.13				
1058	DCHS2	p.S427	4	155411227	155411227 A	G	SNP	tier1	ENSG00000197410	224	1	0.44	101	97	48.99				
1058	BTNL9	p.A328V	5	180485376	180485376 C	T	SNP	tier1	ENSG00000165810	132	0	0	76	60	44.12				
1058	TNXB	p.P1451L	6	32046833	32046833 G	A	SNP	tier1	ENSG00000168477	68	1	1.45	26	16	38.1				
1058	DNAH8	p.F1580	6	38819375	38819375 T	C	SNP	tier1	ENSG00000124721	83	1	1.19	73	5	6.41				
1058	OSTM1	NULL	6	108365474	108365474 G	C	SNP	tier3	ENSG0000081087	130	0	0	90	0	0				
1058	PTPRZ1	e13+29	7	121659351	121659351 T	C	SNP	tier3	ENSG00000106278	74	0	0	39	31	44.29				
1058	EZH2	p.R690C	7	148506444	148506444 G	A	SNP	tier1	ENSG00000106462	242	0	0	192	20	9.35				
1058	EZH2	p.E655K	7	148507491	148507491 C	T	SNP	tier1	ENSG00000106462	158	0	0	54	53	49.53				
1058	EZH2	p.V172	7	148525941	148525941 C	T	SNP	tier1	ENSG00000106462	176	2	1.12	111	3	2.63				
1058	SBF1P1	NULL	8	56367604	56367604 C	T	SNP	tier2	ENSG00000248522	303	1	0.33	255	13	4.83				
1058	RAD21	p.G221*	8	117869533	117869533 C	A	SNP	tier1	ENSG00000164754	461	1	0.22	390	23	5.57				
1058	RAD21	p.R65*	8	117875450	117875450 G	A	SNP	tier1	ENSG00000164754	379	2	0.52	231	96	29.36				
1058	MYO5BP2	NULL	9	66513463	66513463 G	A	SNP	tier3	ENSG00000238245	608	6	0.98	526	68	11.45				
1058	TBX22	p.R126Q	X	79279582	79279582 G	A	SNP	tier1	ENSG00000122145	67	1	1.47	5	54	91.53				
1059	NRAS	p.Q61H	1	115256528	115256528 T	A	SNP	tier1	ENSG00000213281	286	0	0	262	120	31.41				

1059	U2AF1	p.Q157P	21	44514777	44514777 T	G	SNP	tier1	ENSG00000160201	101	0	0	106	99	48.29
1059	ARHGEF16	p.D673	1	3397040	3397040 C	T	SNP	tier1	ENSG00000130762	50	0	0	28	30	51.72
1059	GJB5	p.R32H	1	35223026	35223026 G	A	SNP	tier1	ENSG00000189280	116	2	1.69	83	49	37.12
1059	PLXNA2	e4+13	1	208276479	208276479 A	G	SNP	tier2	ENSG00000076356	61	0	0	51	29	34.94
1059	ENSG00000245832	NULL	11	81601893	81601894 -	T	INS	tier3	ENSG00000245832	69	0	0	90	1	1.1
1059	CBL	p.G415S	11	119149235	119149235 G	A	SNP	tier1	ENSG00000110395	230	3	1.29	183	156	45.88
1059	CCNB2	e4+4	15	59406817	59406817 G	A	SNP	tier3	ENSG00000157456	70	0	0	45	46	50.55
1059	MYO5B	e29+28	18	47389569	47389569 C	T	SNP	tier2	ENSG00000167306	168	6	3.45	93	91	49.46
1059	FCGBP	p.R5232H	19	40357618	40357618 C	T	SNP	tier1	ENSG00000090920	184	1	0.54	168	133	44.04
1059	GATA2	p.P385L	3	128200151	128200151 G	A	SNP	tier1	ENSG00000179348	115	0	0	101	63	38.41
1059	NLGN1	NULL	3	174000648	174000648 G	A	SNP	tier2	ENSG00000169760	79	0	0	26	29	52.73
1059	RUNX1T1	p.T613I	8	92972480	92972480 G	A	SNP	tier1	ENSG00000079102	175	1	0.57	212	91	29.93
1059	NFIB	NULL	9	14305928	14305928 C	T	SNP	tier2	ENSG00000147862	53	0	0	27	24	47.06
1059	C9orf3	NULL	9	97694065	97694065 G	T	SNP	tier3	ENSG00000148120	51	2	3.77	41	23	35.38
1059	STAG2	p.E990*	X	123217314	123217314 G	T	SNP	tier1	ENSG00000101972	112	2	1.75	14	176	92.63
1063	USP24	e2-6	1	55643811	55643811 G	A	SNP	tier3	ENSG00000162402	169	0	0	144	33	18.64
1063	GBP4	p.M70V	1	89662820	89662820 T	C	SNP	tier1	ENSG00000162654	393	0	0	348	70	16.75
1063	FOLH1	p.G490A	11	49179567	49179567 C	G	SNP	tier1	ENSG00000086205	108	0	0	90	12	11.76
1063	TP53	p.E286K	17	7577082	7577082 C	T	SNP	tier1	ENSG00000141510	193	0	0	252	46	15.44
1063	DCAF7	p.T213I	17	61660973	61660973 C	T	SNP	tier1	ENSG00000136485	80	0	0	99	26	20.8
1063	CEACAMP8	NULL	19	43544634	43544634 G	A	SNP	tier3	ENSG00000236932	91	1	1.09	96	19	16.52
1063	ENSG00000204745	NULL	2	87398390	87398390 T	G	SNP	tier2	ENSG00000204745	58	0	0	57	12	17.39
1063	STAT4	e17+95	2	191899179	191899179 T	C	SNP	tier3	ENSG00000138378	90	1	1.08	61	10	13.89
1063	DMRT2	p.H225D	9	1055766	1055766 C	G	SNP	tier1	ENSG00000173253	176	1	0.56	126	23	15.44
1063	UBQLN1	p.S159R	9	86294924	86294924 A	C	SNP	tier1	ENSG00000135018	61	0	0	46	9	16.36
1064	IDH2	p.R140Q	15	90631934	90631934 C	T	SNP	tier1	ENSG00000182054	310	2	0.64	354	29	7.57
1064	LOC388630	p.S406	1	48240973	48240973 G	A	SNP	tier1	ENSG00000204018	81	0	0	52	36	40.91
1064	JUN	NULL	1	59249871	59249871 T	C	SNP	tier3	ENSG00000177606	92	1	1.08	61	46	42.99
1064	CLCA3P	NULL	1	87120369	87120369 C	T	SNP	tier3	ENSG00000153923	56	0	0	43	33	43.42
1064	PAX6	NULL	11	31832994	31832994 A	C	SNP	tier2	ENSG0000007372	89	0	0	87	12	12.12
1064	TAS2R46	p.H212R	12	11214259	11214259 T	C	SNP	tier1	ENSG00000226761	69	0	0	54	32	37.21
1064	ENSG00000256663	NULL	12	20705497	20705497 G	A	SNP	tier2	ENSG00000256663	57	0	0	51	27	33.75
1064	LRRK2	p.A370T	12	40645273	40645273 G	A	SNP	tier1	ENSG00000188906	78	1	1.27	72	32	30.77
1064	SACS	p.T3175A	13	23908492	23908492 T	C	SNP	tier1	ENSG00000151835	97	9	8.49	130	79	37.8
1064	OR4K1	p.G252R	14	20404579	20404579 G	A	SNP	tier1	ENSG00000155249	111	1	0.89	97	34	25.95
1064	LCTL	e7-52	15	66850426	66850426 C	T	SNP	tier3	ENSG00000188501	56	2	3.45	46	40	46.51
1064	UBFD1	NULL	16	23585627	23585627 T	-	DEL	tier2	ENSG00000103353	55	0	0	58	0	0
1064	GPR179	p.T340	17	36493068	36493068 G	A	SNP	tier1	ENSG00000188888	60	2	3.23	50	29	36.71
1064	SRSF2	p.P95R	17	74732959	74732959 G	C	SNP	tier1	ENSG00000161547	140	4	2.78	70	73	50.34
1064	CHAC2	NULL	2	54002244	54002244 G	A	SNP	tier2	ENSG00000143942	89	0	0	78	37	31.9
1064	FSIP2	p.D1984N	2	186657546	186657546 G	A	SNP	tier1	ENSG00000188738	73	0	0	63	9	12.5
1064	PTPRT	p.R364Q	20	41306568	41306568 C	T	SNP	tier1	ENSG00000196090	255	6	2.3	149	123	44.89
1064	RUNX1	p.W279*	21	36171728	36171728 C	T	SNP	tier1	ENSG00000159216	477	7	1.45	285	173	37.77
1064	RUNX1	p.A142fs	21	36252939	36252940 -	TGCCCCTT	INS	tier1	ENSG00000159216	470	5	1.05	379	56	12.87
1064	RRP1	p.L440fs	21	45223584	45223584 C	-	DEL	tier1	ENSG00000160214	66	1	1.49	41	39	48.75
1064	YBEY	e3+9	21	47716153	47716153 C	T	SNP	tier3	ENSG00000182362	118	2	1.67	75	47	38.52
1064	DIP2A	p.T1311	21	47978267	47978267 C	T	SNP	tier1	ENSG00000160305	110	0	0	105	6	5.41
1064	CLDN11	e3-109249	3	170316584	170316584 C	A	SNP	tier3	ENSG0000013297	104	2	1.87	90	55	37.67
1064	MB21D2	p.R230H	3	192516962	192516962 C	T	SNP	tier1	ENSG00000180611	73	2	2.67	45	28	38.36
1064	COX7B2	p.A48V	4	46737067	46737067 G	A	SNP	tier1	ENSG00000170516	76	0	0	52	31	36.9
1064	EDIL3	p.S317L	5	83360521	83360521 G	A	SNP	tier1	ENSG00000164176	315	2	0.63	244	152	38.38
1064	PCDHA6	p.D481V	5	140209118	140209118 A	T	SNP	tier1	ENSG00000081842	422	0	0	399	25	5.9
1064	PCDHB14	p.R461C	5	140604458	140604458 C	T	SNP	tier1	ENSG00000120327	282	7	2.42	176	120	40.4
1064	FLT4	e22+14	5	180043886	180043886 C	T	SNP	tier2	ENSG00000037280	64	0	0	45	36	44.44
1064	GRIK2	p.N897	6	102516350	102516350 C	T	SNP	tier1	ENSG00000164418	338	0	0	401	16	3.84
1064	GLI3	p.N56	7	42188024	42188024 G	A	SNP	tier1	ENSG00000106571	79	1	1.25	69	11	13.75

1064	JPH1	NULL	8	75147127	75147127 T	C	SNP	tier3	ENSG00000104369	80	0	0	58	35	37.63
1064	SLC30A8	p.V181I	8	118170052	118170052 G	A	SNP	tier1	ENSG00000164756	66	0	0	48	15	23.81
1064	CACNA1B	p.G1121S	9	140938297	140938297 G	A	SNP	tier1	ENSG00000148408	287	0	0	302	29	8.76
1064	PHF6	p.R275*	X	133549136	133549136 C	T	SNP	tier1	ENSG00000156531	135	5	3.55	61	133	68.56

Table S4. Mutations identified in 8 gene (AmpliSeq) panel analysis

Patient	Chromosome	Start	Stop	Reference	Variant	Variant				Gene name	EnsemblGeneID	Mutation type	Position	Amino acid change
						Reference Count	Variant Count	Frequency	Allele type					
1002	17	7577548	7577548	C	T	2804	1925	40.68	SNP	TP53	ENST00000269305	missense	c.733	p.G245S
1004	17	7578553	7578553	T	C	30	52	63.41	SNP	TP53	ENST00000269305	missense	c.377	p.Y126C
1010	2	198266834	198266834	T	C	686	609	47.03	SNP	SF3B1	ENST00000335508	missense	c.2098	p.K700E
1010	15	90631838	90631838	C	T	933	749	44.53	SNP	IDH2	ENST00000330062	missense	c.515	p.R172K
1011	17	74732959	74732959	G	C	525	23	4.2	SNP	SRSF2	ENST00000359995	missense	c.284	p.P95R
1013	17	7578203	7578203	C	T	324	1082	76.96	SNP	TP53	ENST00000269305	missense	c.646	p.V216M
1013	17	7578203	7578203	C	T	324	1082	76.96	SNP	TP53	ENST00000269305	missense	c.646	p.V216M
1014	17	7573996	7573996	A	G	537	1562	74.17	SNP	TP53	ENST00000269305	missense	c.1031	p.L344P
1017	17	7577581	7577581	A	T	1212	1643	56.91	SNP	TP53	ENST00000269305	missense	c.700	p.Y234N
1019	17	7578407	7578407	G	C	6	60	90.91	SNP	TP53	ENST00000269305	missense	c.523	p.R175G
1023	17	7577121	7577121	G	A	279	1014	78.3	SNP	TP53	ENST00000269305	missense	c.817	p.R273C
1035	15	90631934	90631934	C	T	1731	210	10.81	SNP	IDH2	ENST00000330062	missense	c.419	p.R140Q
1035	17	74732959	74732959	G	T	538	56	9.43	SNP	SRSF2	ENST00000359995	missense	c.284	p.P95H
1036	2	209113113	209113113	G	A	1226	154	11.16	SNP	IDH1	ENST00000345146	missense	c.394	p.R132C
1037	17	7577120	7577120	C	T	2658	296	10.01	SNP	TP53	ENST00000269305	missense	c.818	p.R273H
1037	20	31022436	31022437	-	G	40	12	23.08	INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.l641fs
1041	20	31022436	31022437	-	G	28	7	20	INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.l641fs
1047	17	7578271	7578271	T	C	1708	265	13.42	SNP	TP53	ENST00000269305	missense	c.578	p.H193R
1048	17	7577094	7577094	G	A	571	1417	70.32	SNP	TP53	ENST00000269305	missense	c.844	p.R282W
1049	2	198266834	198266834	T	C	1468	363	19.8	SNP	SF3B1	ENST00000335508	missense	c.2098	p.K700E
1049	2	209113113	209113113	G	A	1381	177	11.35	SNP	IDH1	ENST00000345146	missense	c.394	p.R132C
1049	20	31022436	31022437	-	G	52	15	22.39	INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.l641fs
1061	2	198267299	198267300	-	A	2596	1111	29.97	INS	SF3B1	ENST00000335508	frame_shift_ins	c.2058_2057	p.L686fs
1062	17	7577511	7577511	A	G	2069	1140	35.2	SNP	TP53	ENST00000269305	missense	c.770	p.L257P
1062	17	7578271	7578271	T	A	1058	832	43.47	SNP	TP53	ENST00000269305	missense	c.578	p.H193L
1063	17	7577082	7577082	C	T	1762	423	19.29	SNP	TP53	ENST00000269305	missense	c.856	p.E286K
1065	17	7579445	7579445	G	-	1599	3662	69.61	DEL	TP53	ENST00000269305	frame_shift_del	c.242	p.T81fs
1066	17	7577539	7577539	G	A	5318	2728	33.69	SNP	TP53	ENST00000269305	missense	c.742	p.R248W
1068	17	7577120	7577120	C	A	3136	1374	29.83	SNP	TP53	ENST00000269305	missense	c.818	p.R273L
1068	17	7578508	7578508	C	T	179	66	26.83	SNP	TP53	ENST00000269305	missense	c.422	p.C141Y
1070	2	198267359	198267359	C	G	1842	1270	40.78	SNP	SF3B1	ENST00000335508	missense	c.1998	p.K666N
1072	17	7578556	7578556	T	G	146	95	39.09	SNP	TP53	ENST00000269305	splice_site	c.376-2	e4-2
1072	17	7579317	7579317	A	G	4285	2304	34.81	SNP	TP53	ENST00000269305	missense	c.370	p.C124R
1072	20	31022450	31022451	-	G	35	10	22.22	INS	ASXL1	ENST00000375687	frame_shift_ins	c.1935_1936	p.G648fs
1073	20	31022436	31022437	-	G	61	16	20.78	INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.l641fs
1074	2	25457242	25457242	C	T	1816	1515	45.45	SNP	DNMT3A	ENST00000264709	missense	c.2645	p.R882H
1074	15	90631934	90631934	C	T	1820	965	34.6	SNP	IDH2	ENST00000330062	missense	c.419	p.R140Q
1076	17	7574018	7574018	G	A	1954	2481	55.9	SNP	TP53	ENST00000269305	missense	c.1009	p.R337C
1078	17	74732959	74732959	G	T	817	442	35.11	SNP	SRSF2	ENST00000359995	missense	c.284	p.P95H
1084	2	25457242	25457242	C	T	2928	1739	37.23	SNP	DNMT3A	ENST00000264709	missense	c.2645	p.R882H
1085	17	7577157	7577157	T	G	3174	2213	40.48	SNP	TP53	ENST00000269305	splice_site	c.783-2	e7-2
1085	17	7577532	7577532	G	A	8705	2139	19.72	SNP	TP53	ENST00000269305	missense	c.749	p.P250L
1088	2	198267299	198267300	-	A	1302	521	28.58	INS	SF3B1	ENST00000335508	frame_shift_ins	c.2058_2057	p.L686fs
1089	17	74732960	74732960	G	C	475	212	30.86	SNP	SRSF2	ENST00000359995	missense	c.283	p.P95A

1090	17	74732959	74732959 G	T	911	628	40.81 SNP	SRSF2	ENST00000359995	missense	c.284	p.P95H
800684	17	7578449	7578449 C	T	45	16	25.81 SNP	TP53	ENST00000269305	missense	c.481	p.A161T
800684	17	7578556	7578556 T	C	57	40	40.4 SNP	TP53	ENST00000269305	splice_site	c.376-2	e4-2
UC1	2	25457242	25457242 C	T	1748	1048	37.47 SNP	DNMT3A	ENST00000264709	missense	c.2645	p.R882H
UC2	20	31022436	31022437 -	G	42	13	23.64 INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.I641fs
UC3	20	31022436	31022437 -	G	15	4	21.05 INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.I641fs
UC5	17	7577527	7577527 G	A	66	11	14.29 SNP	TP53	ENST00000269305	missense	c.754	p.L252F
UC8	20	31022436	31022437 -	G	41	11	21.15 INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.I641fs
UC9	15	90631838	90631838 C	T	2720	484	15.11 SNP	IDH2	ENST00000330062	missense	c.515	p.R172K
UC9	20	31022436	31022437 -	G	32	12	27.27 INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.I641fs
UC10	20	31022436	31022437 -	G	47	19	28.79 INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.I641fs
UC11	2	209113113	209113113 G	A	1177	981	45.44 SNP	IDH1	ENST00000345146	missense	c.394	p.R132C
UC11	20	31022436	31022437 -	G	32	10	23.81 INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.I641fs
UC13	20	31022436	31022437 -	G	20	9	31.03 INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.I641fs
UC14	17	74732959	74732959 G	C	736	584	44.21 SNP	SRSF2	ENST00000359995	missense	c.284	p.P95R
UC15	2	198266828	198266828 G	T	1426	1350	48.21 SNP	SF3B1	ENST00000335508	silent	c.2104	p.R702
UC15	15	90631838	90631838 C	T	1909	1257	39.7 SNP	IDH2	ENST00000330062	missense	c.515	p.R172K
UC15	20	31022436	31022437 -	G	36	10	21.74 INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.I641fs
UC16	17	74732959	74732959 G	T	130	63	32.64 SNP	SRSF2	ENST00000359995	missense	c.284	p.P95H
UC17	20	31022436	31022437 -	G	21	9	30 INS	ASXL1	ENST00000375687	frame_shift_ins	c.1921_1922	p.I641fs
UC22	17	74732959	74732959 G	T	720	444	38.14 SNP	SRSF2	ENST00000359995	missense	c.284	p.P95H
UC24	17	74732959	74732959 G	T	550	441	44.46 SNP	SRSF2	ENST00000359995	missense	c.284	p.P95H
UC26	15	90631934	90631934 C	T	1309	1170	47.16 SNP	IDH2	ENST00000330062	missense	c.419	p.R140Q
UC26	17	74732959	74732959 G	C	448	282	38.63 SNP	SRSF2	ENST00000359995	missense	c.284	p.P95R
UC26	20	31022459	31022460 -	G	16	5	23.81 INS	ASXL1	ENST00000375687	frame_shift_ins	c.1944_1945	p.G649fs

Table S5. Somatic, nonsynonymous TP53 mutations

Patient	Blast count	Gene	Amino Acid Change					Tumor Reference Count	Tumor Variant Count	Tumor Variant Allele Frequency	Number of times variant noted in Cosmic, Haematopoietic neoplasm*	Number of times variant noted in Cosmic, Confirmed Somatic**	
			Start	Stop	Reference	Variant	LOH						
1002	24%	TP53	p.G245S	7577548	7577548	C	T	2804	1925	40.7	6	102	
1004	57%	TP53	p.Y126C	7578553	7578553	T	C	48	95	66.4	1	8	
1013	57%	TP53	p.V216M	7578203	7578203	C	T	324	1082	77.0	8	31	
1014	8%	TP53	p.L344P	7573996	7573996	A	G	537	1562	74.2	0	3	
1017	40%	TP53	p.Y234N	7577581	7577581	A	T	1212	1643	56.9	0	5	
1019	9%	TP53	p.R175G	7578407	7578407	G	C	6	60	90.9	0	11	
1023	10%	TP53	p.R273C	7577121	7577121	G	A	279	1014	78.3	8	219	
1037	20%	TP53	p.H179P	7578394	7578394	T	G	592	73	10.9	0	1	
1037	20%	TP53	p.R273H	7577120	7577120	C	T	2658	296	10.0	5	241	
1047	7%	TP53	p.H193R	7578271	7578271	T	C	1708	265	13.4	4	41	
1048	55%	TP53	p.R282W	7577094	7577094	G	A	571	1417	70.3	1	179	
1062	27%	TP53	p.H193L	7578271	7578271	T	A	1058	832	43.5	0	22	
1062	27%	TP53	p.L257P	7577511	7577511	A	G	2069	1140	35.2	0	5	
1063	10%	TP53	p.E286K	7577082	7577082	C	T	1762	423	19.3	0	47	
1065	14%	TP53	p.T81fs	7579445	7579445	G	-	LOH	1599	3662	69.6	0	1
1066	3%	TP53	p.R248W	7577539	7577539	G	A	5318	2728	33.7	8	177	
1068	10%	TP53	p.C141Y	7578508	7578508	C	T	179	66	26.8	2	20	
1068	10%	TP53	p.R273L	7577120	7577120	C	A	3136	1374	29.8	0	70	
1072	30%	TP53	p.C124R	7579317	7579317	A	G	4285	2304	34.8	0	4	
1072	30%	TP53	e4-2	7578556	7578556	T	G	146	95	39.1	0	18	
1076	70%	TP53	p.R337C	7574018	7574018	G	A	LOH	1954	2481	55.9	2	19
1085	12%	TP53	p.P250L	7577532	7577532	G	A	8705	2139	19.7	0	20	
1085	12%	TP53	e7-2	7577157	7577157	T	G	3174	2213	40.5	0	4	
790809	10%	TP53	e4-1	7578555	7578555	C	T	341	38	10.0	1	35	
800684	29%	TP53	e4-2	7578556	7578556	T	C	190	153	44.4	0	18	
800684	29%	TP53	p.A161T	7578449	7578449	C	T	370	252	40.5	0	17	
UC5	15%	TP53	p.L252F	7577527	7577527	G	A	66	11	14.3	0	1	
1080	29%						LOH						

* N = 354 variants, excludes lymphoid malignancies

** N = 7572 variants

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